

SEQUENCE LISTING

<110> Mendel Biotechnology, Inc.
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<120> PLANT TRANSCRIPTIONAL REGULATORS OF DROUGHT STRESS

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 <151> 2003-04-10

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Gly Thr Arg Asp Arg Leu Trp Leu Gly Ser Phe Ser Thr Ala Glu Gly
35          40          45

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Ala Ala Val Ala His Asp Val Ala Phe Phe Cys Leu His Gln Pro Asp
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Ser Leu Glu Ser Leu Asn Phe Pro His Leu Leu Asn Pro Ser Leu Val
65          70          75          80

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Met Ala Ile Asp Ala Gly Ile Val His Ser Thr Ser Val Asn Ser Gly
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20 25 30

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35 40 45

Glu Arg Gly Leu Tyr Leu Ile His Leu Leu Leu Thr Cys Ala Asn His
50 55 60

Val Ala Ser Gly Ser Leu Gln Asn Ala Asn Ala Ala Leu Glu Gln Leu
65 70 75 80

Ser His Leu Ala Ser Pro Asp Gly Asp Thr Met Gln Arg Ile Ala Ala
85 90 95

Tyr Phe Thr Glu Ala Leu Ala Asn Arg Ile Leu Lys Ser Trp Pro Gly
100 105 110

Leu Tyr Lys Ala Leu Asn Ala Thr Gln Thr Arg Thr Asn Asn Val Ser
115 120 125

Glu Glu Ile His Val Arg Arg Leu Phe Phe Glu Met Phe Pro Ile Leu
130 135 140

Lys Val Ser Tyr Leu Leu Thr Asn Arg Ala Ile Leu Glu Ala Met Glu
145 150 155 160

Gly Glu Lys Met Val His Val Ile Asp Leu Asp Ala Ser Glu Pro Ala

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165                               170                               175
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195                               200                               205
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290                               295                               300
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305                               310                               315
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325                               330                               335
Trp Gly Leu Ser Pro Lys Val Met Val Val Thr Glu Gln Asp Ser Asp
340                               345                               350
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355                               360                               365
Tyr Ala Ala Leu Phe Asp Cys Leu Glu Thr Lys Val Pro Arg Thr Ser
370                               375                               380
Gln Asp Arg Ile Lys Val Glu Lys Met Leu Phe Gly Glu Glu Ile Lys
385                               390                               395
Asn Ile Ile Ser Cys Glu Gly Phe Glu Arg Arg Glu Arg His Glu Lys
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Pro Leu Ser Tyr Tyr Ala Met Leu Gln Ala Arg Arg Leu Leu Gln Gly
435 440 445

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25

30

Met Phe Phe Asp Ile Asp Glu Gly Gly Asn Asn Gly Leu Ile Glu Glu
 35 40 45

Glu Ile Ser Ser Pro Thr Ser Ile Val Ser Ser Glu Thr Phe Thr Gly
 50 55 60

Glu Ser Gly Gly Ser Gly Ser Ala Thr Thr Leu Ser Lys Lys Glu Ser
 65 70 75 80

Thr Asn Arg Gly Ser Lys Glu Ser Asp Gln Thr Lys Glu Thr Gly His
 85 90 95

Arg Val Ala Phe Arg Thr Arg Ser Lys Ile Asp Val Met Asp Asp Gly
 100 105 110

Phe Lys Trp Arg Lys Tyr Gly Lys Lys Ser Val Lys Asn Asn Ile Asn
 115 120 125

Lys Arg Asn Tyr Tyr Lys Cys Ser Ser Glu Gly Cys Ser Val Lys Lys
 130 135 140

Arg Val Glu Arg Asp Gly Asp Asp Ala Ala Tyr Val Ile Thr Thr Tyr
 145 150 155 160

Glu Gly Val His Asn His Glu Ser Leu Ser Asn Val Tyr Tyr Asn Glu
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Met Val Leu Ser Tyr Asp His Asp Asn Trp Asn Gln His Ser Leu Leu
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Arg Ser

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caagcaagct cgtttccggg gagttcgaag aaggccttgg ggaaagtttg cagcagagat 180

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Ala Glu Ile Arg Asp Pro Ser Arg Asn Gly Ala Arg Leu Trp Leu Gly
          35          40          45

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Thr Phe Glu Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Arg Ala Ala
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Phe Asn Leu Arg Gly His Leu Ala Ile Leu Asn Phe Pro Asn Glu Tyr
65          70          75          80

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Tyr Pro Arg Met Asp Asp Tyr Ser Leu Arg Pro Pro Tyr Ala Ser Ser
          85          90          95

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Ser Ser Ser Ser Ser Ser Gly Ser Thr Ser Thr Asn Val Ser Arg Gln
          100          105          110

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Asn Gln Arg Glu Val Phe Glu Phe Glu Tyr Leu Asp Asp Lys Val Leu
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Val Val Asp Tyr Leu Arg Pro Lys Asn Ser Asp Arg Asp Thr Ser His
20           25           30

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Val Asp Arg Val Ile Ser Thr Val Thr Ile Arg Ser Phe Asp Pro Trp

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Glu Leu Pro Cys Gln Ser Arg Ile Lys Leu Lys Asp Glu Ser Trp Cys
50 55 60

Phe Phe Ser Pro Lys Glu Asn Lys Tyr Gly Arg Gly Asp Gln Gln Ile
65 70 75 80

Arg Lys Thr Lys Ser Gly Tyr Trp Lys Ile Thr Gly Lys Pro Lys Pro
85 90 95

Ile Leu Arg Asn Arg Gln Glu Ile Gly Glu Lys Lys Val Leu Met Phe
100 105 110

Tyr Met Ser Lys Glu Leu Gly Gly Ser Lys Ser Asp Trp Val Met His
115 120 125

Glu Tyr His Ala Phe Ser Pro Thr Gln Met Met Met Thr Tyr Thr Ile
130 135 140

Cys Lys Val Met Phe Lys Gly Asp Val Arg Glu Ile Ser Ser Ser Ser
145 150 155 160

Ala Ser Tyr Gly Ser Glu Ile Glu Gln Ser Arg Asp Ser Leu Ile Pro
165 170 175

Leu Leu Val Asn Asp Ser Glu Glu Glu Ala Gln Ile Glu Asp Ala Ile
180 185 190

Pro Ile Glu Glu Trp Glu Thr Trp Leu Thr Asp Asp Gly Val Asp Glu
195 200 205

Gln Val Asn His Ile Met Asn Met Lys Asp Asp Arg Asn Asn His Arg
210 215 220

Pro Gln Lys Pro Leu Thr Gly Val Leu Ile Asp Asp Ser Ser Asp Asp
225 230 235 240

Asp Asp Asp Ser Asp Leu Leu Ser Pro Thr Thr Asn Ser Ile Glu Asn
245 250 255

Ser Ser Thr Cys Asp Ser Phe Gly Ser Ser Asp Gln Ile Asn Leu Val
260 265 270

Ser Leu Thr Gln Glu Val Ser Gln Ala Leu Ile Thr Ser Ile Asp Thr
275 280 285

Pro Glu Lys Ile Lys Ser Pro Tyr Asp Asp Ala Gln Gly Thr Gly Ala
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290

295

300

Gly Gly Gln Lys Leu Gly Gln Glu Thr Arg Glu Lys Lys Arg Ala Gly
305 310 315 320

Phe Phe His Arg Met Ile Gln Ile Phe Val Lys Lys Ile His Gln Cys
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<220>
<223> G2133 Predicted polypeptide sequence is paralogous to G47

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<223> G2133 polypeptide Paralogous to G47

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20 25 30

Gly Thr Arg Gln Arg Leu Trp Leu Gly Ser Phe Ser Thr Ala Glu Gly
35 40 45

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Ala Ala Val Ala His Asp Val Ala Phe Tyr Cys Leu His Arg Pro Ser
50 55 60

Ser Leu Asp Asp Glu Ser Phe Asn Phe Pro His Leu Leu Thr Thr Ser
65 70 75 80

Leu Ala Ser Asn Ile Ser Pro Lys Ser Ile Gln Lys Ala Ala Ser Asp
85 90 95

Ala Gly Met Ala Val Asp Ala Gly Phe His Gly Ala Val Ser Gly Ser
100 105 110

Gly Gly Cys Glu Glu Arg Ser Ser Met Ala Asn Met Glu Glu Glu Asp
115 120 125

Lys Leu Ser Ile Ser Val Tyr Asp Tyr Leu Glu Asp Asp Leu Val
130 135 140

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<212> DNA

<213> Arabidopsis thaliana

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<223> G2999 reference sequence; clade identifier

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cctccgtaca cttactccca aaccgccaac aaagagaaac ccaccaccaa aagaaacggg	180
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aagaatcacg cggcgagctc cgggtggacac gttgtcgacg gttgcggcga gtttatgtct	360
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cagagaccac tcggaagccg ccacgtgtct ccgataatga tgagttttgg tgggtggtggt	540
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tatggagtggt atcagtttca tcattatcaa cccaagaaac ggtttaggac aaagttaaat	660
gaagaacaga aggagaagat gatggagttt gctgagaaga ttggttggag aatgacaaaa	720
ctagaagatg atgaagtga tgggttttgt cgtgagatta aagttaaaag acaagtgttt	780
aaagtttggg tgcacaacaa taaacaagca gcaaagaaga aggatattgta agagatttct	840
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Lys Ser Ser Ala Leu Asp His His Arg Leu Pro Pro Tyr Thr Tyr Ser
          20          25          30

Gln Thr Ala Asn Lys Glu Lys Pro Thr Thr Lys Arg Asn Gly Ser Asp
          35          40          45

Pro Asp Pro Asp Pro Asp Leu Asp Thr Asn Pro Ile Ser Ile Ser His
          50          55          60

Ala Pro Arg Ser Tyr Ala Arg Pro Gln Thr Thr Ser Pro Gly Lys Ala
65          70          75          80

Arg Tyr Arg Glu Cys Gln Lys Asn His Ala Ala Ser Ser Gly Gly His
          85          90          95

Val Val Asp Gly Cys Gly Glu Phe Met Ser Ser Gly Glu Glu Gly Thr
          100          105          110

Val Glu Ser Leu Leu Cys Ala Ala Cys Asp Cys His Arg Ser Phe His
          115          120          125

Arg Lys Glu Ile Asp Gly Leu Phe Val Val Asn Phe Asn Ser Phe Gly
          130          135          140

His Ser Gln Arg Pro Leu Gly Ser Arg His Val Ser Pro Ile Met Met
145          150          155          160

Ser Phe Gly Gly Gly Gly Gly Cys Ala Ala Glu Ser Ser Thr Glu Asp
          165          170          175

Leu Asn Lys Phe His Gln Ser Phe Ser Gly Tyr Gly Val Asp Gln Phe
          180          185          190

His His Tyr Gln Pro Lys Lys Arg Phe Arg Thr Lys Phe Asn Glu Glu
          195          200          205

Gln Lys Glu Lys Met Met Glu Phe Ala Glu Lys Ile Gly Trp Arg Met

```

210

215

220

Thr Lys Leu Glu Asp Asp Glu Val Asn Arg Phe Cys Arg Glu Ile Lys
225 230 235 240

Val Lys Arg Gln Val Phe Lys Val Trp Met His Asn Asn Lys Gln Ala
245 250 255

Ala Lys Lys Lys Asp Leu
260

<210> 15
<211> 1621
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G3086 reference sequence; clade identifier

<400> 15
aagtttctct cacgttctct tttttaattt taatttctcg ccggaacaa tctcatctcc 60
cggcgaacga aacttccggt gtggtactgc aaacggagaa aaaaataacc aaagaagaga 120
gaaactcaaa agctactaag atggaatcag aattccagca acatcacttc cttctccacg 180
atcatcaaca ccagagacca agaaactcag gattgattcg ttaccaatca gcaccaagtt 240
cgtacttttc gagtttcggt gaatcaatcg aagagttttt agatcgaccc acaagtcctg 300
aaactgagcg aatcttatct ggctttttac aaaccaccga cacaagcgac aacgttgata 360
gtttccttca ccatactttt aacagtgatg gaactgagaa gaaacctccg gaagttaaaa 420
cagaggacga agatgctgaa attccggtga ctgcgacggc gacggcgatg gaggttggtg 480
tttccggtga tggtgaaatc tcagtgaatc ctgaagtatc gattgggtat gtggcttcgg 540
tttcgaggaa taagagacca agagagaaag atgatcggac tccggtgaat aatctagctc 600
gtcataatag ttcaccggcc ggattatttt catccattga tgttgaaaca gcttatgcag 660
ctgtaatgaa aagtatggga ggttttgag gaagtaatgt gatgagtaca agcaatactg 720
aagcttcgtc tcttactcct agaagcaagt tacttctcc tacttctaga gcgatgagtc 780
cgatctctga ggttgatggt aaaccgggtt tctcgtctag attgcctcct cggacgcttt 840
ccggtggggt taatcgttct tttgggaatg aagggtctgc ttcttccaag cttacagctc 900
ttgctaggac ccaatctgga ggtctagatc aatacaaaac caaggatgag gattcagcaa 960
gtagacgtcc tcctttggca catcacatga gtttgcccaa gtctttatca gatattgaac 1020
agttactgtc agattctatc ccatgtaaga tcagagccaa gcgggggtgt gcaactcatc 1080
ctcgaagcat agccgagagg gtgagaagaa ccaagatcag tgaaagaatg aggaagctgc 1140
aagaccttgt tccaaacatg gacacgcaaa caaacacagc agacatgttg gatcttgccg 1200

MBI0058CIP.ST25.txt

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gagttgtgca tagaagtatc ggttcggcct ttggagaaaa gtcgaagata gcaaagtaga 1380
gaagagatca tgaacaaagc taaatttggt ggtggtggtg aaaaggggttt ttgtaaagtt 1440
ggaacctttt tttggtaggg aagaaagtag caaggttgtg taatgggccg aactccaatg 1500
ctattgtatg ttcttacatc caaaaaaag aaaagcagaa gagaagtgat gtacaatgag 1560
aagcttattt tattgttaact caagaataat tcaggtaatt agtttaaaaa aaaaaaaaaa 1620
a 1621

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<210> 16

<211> 379

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G3086 polypeptide reference sequence; clade identifier

<400> 16

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Met Glu Ser Glu Phe Gln Gln His His Phe Leu Leu His Asp His Gln
1           5           10          15

```

```

His Gln Arg Pro Arg Asn Ser Gly Leu Ile Arg Tyr Gln Ser Ala Pro
          20          25          30

```

```

Ser Ser Tyr Phe Ser Ser Phe Gly Glu Ser Ile Glu Glu Phe Leu Asp
          35          40          45

```

```

Arg Pro Thr Ser Pro Glu Thr Glu Arg Ile Leu Ser Gly Phe Leu Gln
          50          55          60

```

```

Thr Thr Asp Thr Ser Asp Asn Val Asp Ser Phe Leu His His Thr Phe
65          70          75          80

```

```

Asn Ser Asp Gly Thr Glu Lys Lys Pro Pro Glu Val Lys Thr Glu Asp
          85          90          95

```

```

Glu Asp Ala Glu Ile Pro Val Thr Ala Thr Ala Thr Ala Met Glu Val
          100          105          110

```

```

Val Val Ser Gly Asp Gly Glu Ile Ser Val Asn Pro Glu Val Ser Ile
          115          120          125

```

```

Gly Tyr Val Ala Ser Val Ser Arg Asn Lys Arg Pro Arg Glu Lys Asp
          130          135          140

```

```

Asp Arg Thr Pro Val Asn Asn Leu Ala Arg His Asn Ser Ser Pro Ala

```

```

145              150              155              160
Gly Leu Phe Ser Ser Ile Asp Val Glu Thr Ala Tyr Ala Ala Val Met
      165              170              175
Lys Ser Met Gly Gly Phe Gly Gly Ser Asn Val Met Ser Thr Ser Asn
      180              185              190
Thr Glu Ala Ser Ser Leu Thr Pro Arg Ser Lys Leu Leu Pro Pro Thr
      195              200              205
Ser Arg Ala Met Ser Pro Ile Ser Glu Val Asp Val Lys Pro Gly Phe
      210              215              220
Ser Ser Arg Leu Pro Pro Arg Thr Leu Ser Gly Gly Phe Asn Arg Ser
      225              230              235
Phe Gly Asn Glu Gly Ser Ala Ser Ser Lys Leu Thr Ala Leu Ala Arg
      245              250              255
Thr Gln Ser Gly Gly Leu Asp Gln Tyr Lys Thr Lys Asp Glu Asp Ser
      260              265              270
Ala Ser Arg Arg Pro Pro Leu Ala His His Met Ser Leu Pro Lys Ser
      275              280              285
Leu Ser Asp Ile Glu Gln Leu Leu Ser Asp Ser Ile Pro Cys Lys Ile
      290              295              300
Arg Ala Lys Arg Gly Cys Ala Thr His Pro Arg Ser Ile Ala Glu Arg
      305              310              315
Val Arg Arg Thr Lys Ile Ser Glu Arg Met Arg Lys Leu Gln Asp Leu
      325              330              335
Val Pro Asn Met Asp Thr Gln Thr Asn Thr Ala Asp Met Leu Asp Leu
      340              345              350
Ala Val Gln Tyr Ile Lys Asp Leu Gln Glu Gln Val Lys Ala Leu Glu
      355              360              365
Glu Ser Arg Ala Arg Cys Arg Cys Ser Ser Ala
      370              375

```

```

<210> 17
<211> 553
<212> DNA
<213> Arabidopsis thaliana

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<220>

<223> G30 Predicted polypeptide sequence is paralogous to G1792

<400> 17

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ctctttctgac gcacaacagt atatacacat acacagatat atggatcaag gaggtcgtag      60
cagtggtagt ggaggaggag gagccgagca aggggaagtac cgtggagtaa ggagacgacc    120
ttggggtaaaa tacgccgcgg aaataagaga ttcgaggaag cacggagagc gtgtgtggct    180
agggacattc gacactgcgg aagacgcggc tcgagcctat gaccgagccg cctattcaat    240
gagaggcaaaa gctgccattc tcaacttccc tcacgagtat aacatgggaa ccggatcctc    300
atccactgcg gctaattctt cttcctcgtc gcagcaagtt tttgagtttg agtacttgga    360
cgatagcggtt ttggatgaac ttcttgaata tggagagaac tataacaaga ctcataatat    420
caacatgggc aagaggcaat aaaggaata caatcggtat taactgaaag ttatgtgaaa    480
gaccattttc agttataaca aataaaataa aatcccaagc gtacaaagct gtttctaaaa    540
aaaaaaaaaa aaa                                                         553

```

<210> 18

<211> 133

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G30 polypeptide Paralogous to G1792

<400> 18

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Met Asp Gln Gly Gly Arg Ser Ser Gly Ser Gly Gly Gly Ala Glu
1          5          10          15

```

```

Gln Gly Lys Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Tyr Ala
          20          25          30

```

```

Ala Glu Ile Arg Asp Ser Arg Lys His Gly Glu Arg Val Trp Leu Gly
          35          40          45

```

```

Thr Phe Asp Thr Ala Glu Asp Ala Ala Arg Ala Tyr Asp Arg Ala Ala
          50          55          60

```

```

Tyr Ser Met Arg Gly Lys Ala Ala Ile Leu Asn Phe Pro His Glu Tyr
          65          70          75          80

```

```

Asn Met Gly Thr Gly Ser Ser Ser Thr Ala Ala Asn Ser Ser Ser Ser
          85          90          95

```

```

Ser Gln Gln Val Phe Glu Phe Glu Tyr Leu Asp Asp Ser Val Leu Asp
          100          105          110

```

```

Glu Leu Leu Glu Tyr Gly Glu Asn Tyr Asn Lys Thr His Asn Ile Asn

```

Met Gly Lys Arg Gln
130

<210> 19
<211> 1462
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G515 Predicted polypeptide sequence is paralogous to G2053

<400> 19
caaccatggc gaaagctctc caatgcatat ttttttgatc ttttcctttt cccttctttt 60
ttgatcgctg cagagaaatg gaaactcctg tgggtttaag attctgtccg accgacgagg 120
agatcgctcg cgattacctt tggccgaaaa attccgatag agacacgagc catgtcgatc 180
gattcattaa cacagtccct gtctgtagac tcgatccttg ggagttacct tgccagtcaa 240
ggatcaaaact gaaagatgtg gcttggtggt tcttcagacc taaggagaac aaatatggca 300
gaggtgatca gcagatgaga aaaacgaaat ctgggttttg gaagagtact ggcagaccaa 360
agcctatcat gcgtaatcgc caacagatcg gtgagaaaaa gattttgatg ttttacacga 420
gtaaggaatc caaatccgat tgggttatac acgagtacca cggtttctct cataaccaga 480
tgatgatgac atacacactc tgtaaagtta tgtttaaatgg tggcatgaga gagaagtctt 540
cctcttctcc ttcttcttct ggtgtagtg gaattgagca gagtcgtcgt gactctttaa 600
tccttcagct tgtcaacaat tctgagggat cctcacttca cagagaagat ccaagtcagt 660
ttggtgatgt gctgcaagaa gctccaatcg aggatgctaa actgaccgag gaattggtaa 720
aatggctgat gaatgatgag gatgatgctc aaatcgagga tgctataccg attgaggaat 780
gggaaacatg gttgaatgat attgatgatg ctaaggagaa gagtatcatg tttatgcatg 840
ataatcgaag tgattacaga cctccaaact cattaactgg tgtcttcagt gatgatgtta 900
gcagtgatga taatgattct gatttgctaa ctccaaaaac aaactctatt caaacttcga 960
gcacttgatga tagttttggt agctcaaatc atcgcataga ccagatcaaa gacctgcaag 1020
aatctcctac ctcaacaatc aacttagtgt cactaactca agaggtgagc caagctctaa 1080
taaccagtat tgataccgcc gagaagaaga agaatcctta tgatgatgca caagggactg 1140
agattggtga gcataaattg ggtcaagaga cgatcaagaa gaaaagagct ggtttctttc 1200
acaggatgat acaaaaattc gtcaagaaaa ttcacctatg ttcttccatc tcaagaactt 1260
gataacaata aaagtgatca ataacacctt ttctactttc caaattattht acaacagtac 1320
aagtgtatgc tatgatgtct atcttggttt gtaactttac catactgtat gtgtgatatg 1380
tataaaactg gtaaatttgt gaagacaaat ttgtatccat tgacataata atgtctatct 1440

tgttttgtta aaaaaaaaaa aa

1462

<210> 20

<211> 394

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G515 polypeptide Paralogous to G2053

<400> 20

Met Glu Thr Pro Val Gly Leu Arg Phe Cys Pro Thr Asp Glu Glu Ile
 1 5 10 15

Val Val Asp Tyr Leu Trp Pro Lys Asn Ser Asp Arg Asp Thr Ser His
 20 25 30

Val Asp Arg Phe Ile Asn Thr Val Pro Val Cys Arg Leu Asp Pro Trp
 35 40 45

Glu Leu Pro Cys Gln Ser Arg Ile Lys Leu Lys Asp Val Ala Trp Cys
 50 55 60

Phe Phe Arg Pro Lys Glu Asn Lys Tyr Gly Arg Gly Asp Gln Gln Met
 65 70 75 80

Arg Lys Thr Lys Ser Gly Phe Trp Lys Ser Thr Gly Arg Pro Lys Pro
 85 90 95

Ile Met Arg Asn Arg Gln Gln Ile Gly Glu Lys Lys Ile Leu Met Phe
 100 105 110

Tyr Thr Ser Lys Glu Ser Lys Ser Asp Trp Val Ile His Glu Tyr His
 115 120 125

Gly Phe Ser His Asn Gln Met Met Met Thr Tyr Thr Leu Cys Lys Val
 130 135 140

Met Phe Asn Gly Gly Met Arg Glu Lys Ser Ser Ser Ser Pro Ser Ser
 145 150 155 160

Ser Gly Val Ser Gly Ile Glu Gln Ser Arg Arg Asp Ser Leu Ile Pro
 165 170 175

Gln Leu Val Asn Asn Ser Glu Gly Ser Ser Leu His Arg Glu Asp Pro
 180 185 190

Ser Gln Phe Gly Asp Val Leu Gln Glu Ala Pro Ile Glu Asp Ala Lys
 195 200 205

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Leu Thr Glu Glu Leu Val Lys Trp Leu Met Asn Asp Glu Asp Asp Ala
210 215 220

Gln Ile Glu Asp Ala Ile Pro Ile Glu Glu Trp Glu Thr Trp Leu Asn
225 230 235 240

Asp Ile Asp Asp Ala Lys Glu Lys Ser Ile Met Phe Met His Asp Asn
245 250 255

Arg Ser Asp Tyr Arg Pro Pro Asn Ser Leu Thr Gly Val Phe Ser Asp
260 265 270

Asp Val Ser Ser Asp Asp Asn Asp Ser Asp Leu Leu Thr Pro Lys Thr
275 280 285

Asn Ser Ile Gln Thr Ser Ser Thr Cys Asp Ser Phe Gly Ser Ser Asn
290 295 300

His Arg Ile Asp Gln Ile Lys Asp Leu Gln Glu Ser Pro Thr Ser Thr
305 310 315 320

Ile Asn Leu Val Ser Leu Thr Gln Glu Val Ser Gln Ala Leu Ile Thr
325 330 335

Ser Ile Asp Thr Ala Glu Lys Lys Lys Asn Pro Tyr Asp Asp Ala Gln
340 345 350

Gly Thr Glu Ile Gly Glu His Lys Leu Gly Gln Glu Thr Ile Lys Lys
355 360 365

Lys Arg Ala Gly Phe Phe His Arg Met Ile Gln Lys Phe Val Lys Lys
370 375 380

Ile His Leu Cys Ser Ser Ile Ser Arg Thr
385 390

<210> 21

<211> 1053

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G516 Predicted polypeptide sequence is paralogous to G2053

<400> 21

atggcgaatc cgggtgggttt tagattccgt ccgactgacg gggagatcgt cgacatttac 60

ctccgaccga aaaatctcga aagtaacacg agccatgtcg atgaagtcac tagcacagtt 120

gatatttgta gcttcgaccc ttgggactta ccttcccatt ctaggatgaa aacaagagat 180

MBI0058CIP.ST25.txt

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cagggtttggt atttcttcgg ccgtaaggag aacaaatatg gtaaagggtga tcgacagata 240
agaaaaacca agtctggttt ttggaagaaa actggcggtta ccatggatat aatgcgcaaa 300
acgggagatc gtgagaagat cggtgagaaa aggggttttg tgtttaagaa tcacggtggt 360
tccaagtccg attgggctat gcatgagtat cacgctacgt tctcgtctcc taatcagggt 420
gaaaggagag aattttcagt tgctactggt agtggaatta agcatactca ctctttaatc 480
cctcctacca acaattctgg agttttgagt gtagagacag agggatcggt gtttcacagc 540
caagaatcac agaatccaag tcagttttct ggctttcttg atgtggatgc actagatagg 600
gacttctgca atattttgag tgatgatttc aaaggcttct ttaatgatga cgatgagcag 660
agtaagattg tttctatgca agatgatcgc aacaaccaca cacctcaaaa gccattgacc 720
gggtgtcttca gtgatcatag caccgatggt agtgattctg atccgatttc tgcaacaact 780
atttccattc aaactttaag cacttgctct agttttggta gctcaaattc tctataccaa 840
atcactgact tgcaggaatc tcctaactca atcaagttag tgtcattagc tcaagagggtg 900
agcaaaacac cgggaaccgg tattgataat gatgcacaag ggactgagat tgggtgagcat 960
aaattgggtc aagagacgat caagaacaaa agagctgggt tctttcacag gatgatacaa 1020
aaattcgtca agaaaattca cctaagaaca tga 1053

```

```

<210> 22
<211> 350
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G516 polypeptide Paralogous to G2053

<400> 22

```

```

Met Ala Asn Pro Val Gly Phe Arg Phe Arg Pro Thr Asp Gly Glu Ile
1           5           10           15

```

```

Val Asp Ile Tyr Leu Arg Pro Lys Asn Leu Glu Ser Asn Thr Ser His
          20           25           30

```

```

Val Asp Glu Val Ile Ser Thr Val Asp Ile Cys Ser Phe Asp Pro Trp
          35           40           45

```

```

Asp Leu Pro Ser His Ser Arg Met Lys Thr Arg Asp Gln Val Trp Tyr
          50           55           60

```

```

Phe Phe Gly Arg Lys Glu Asn Lys Tyr Gly Lys Gly Asp Arg Gln Ile
65           70           75           80

```

```

Arg Lys Thr Lys Ser Gly Phe Trp Lys Lys Thr Gly Val Thr Met Asp
          85           90           95

```

MBI0058CIP.ST25.txt

Ile Met Arg Lys Thr Gly Asp Arg Glu Lys Ile Gly Glu Lys Arg Val
100 105 110

Leu Val Phe Lys Asn His Gly Gly Ser Lys Ser Asp Trp Ala Met His
115 120 125

Glu Tyr His Ala Thr Phe Ser Ser Pro Asn Gln Gly Glu Arg Arg Glu
130 135 140

Phe Ser Val Ala Thr Gly Ser Gly Ile Lys His Thr His Ser Leu Ile
145 150 155 160

Pro Pro Thr Asn Asn Ser Gly Val Leu Ser Val Glu Thr Glu Gly Ser
165 170 175

Leu Phe His Ser Gln Glu Ser Gln Asn Pro Ser Gln Phe Ser Gly Phe
180 185 190

Leu Asp Val Asp Ala Leu Asp Arg Asp Phe Cys Asn Ile Leu Ser Asp
195 200 205

Asp Phe Lys Gly Phe Phe Asn Asp Asp Asp Glu Gln Ser Lys Ile Val
210 215 220

Ser Met Gln Asp Asp Arg Asn Asn His Thr Pro Gln Lys Pro Leu Thr
225 230 235 240

Gly Val Phe Ser Asp His Ser Thr Asp Gly Ser Asp Ser Asp Pro Ile
245 250 255

Ser Ala Thr Thr Ile Ser Ile Gln Thr Leu Ser Thr Cys Pro Ser Phe
260 265 270

Gly Ser Ser Asn Pro Leu Tyr Gln Ile Thr Asp Leu Gln Glu Ser Pro
275 280 285

Asn Ser Ile Lys Leu Val Ser Leu Ala Gln Glu Val Ser Lys Thr Pro
290 295 300

Gly Thr Gly Ile Asp Asn Asp Ala Gln Gly Thr Glu Ile Gly Glu His
305 310 315 320

Lys Leu Gly Gln Glu Thr Ile Lys Asn Lys Arg Ala Gly Phe Phe His
325 330 335

Arg Met Ile Gln Lys Phe Val Lys Lys Ile His Leu Arg Thr
340 345 350

<210> 23
 <211> 1080
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <223> G517 Predicted polypeptide sequence is paralogous to G2053

<400> 23
 atgatgaatc cgggtgggttt cagattccgt ccaaacgacg aggagatcgt cgaccattac 60
 ctccggccaa aaaatctcga tagtgacact agccatgtcg atgaagtcac tagcacagtc 120
 gatattctgta gcttcgagcc ttgggattta ccttccaagt cgatgatcaa atcgagagat 180
 ggggttttgt atttcttttag tgttaaggag atgaagtata acagagggtga tcaacagaga 240
 agaagaacaa actctggggt ttggaagaaa actggaaaaa caatgactgt catgcgcaaa 300
 agaggaaatc gtgagaagat cggtgagaaa aggggttttg tttttaagaa tcgagatggg 360
 tcaaagaccg actgggttat gcacgagtat cacgctacgt ccttgtttcc taatcagatg 420
 atgacgtata cagtctgcaa agttgagttt aagggtgaag agacagagat ctcttcttct 480
 tctactggta gtgaaattga acagattcac tctttaatcc ctcttgtaa cagttctgga 540
 ggatctgagg gttcgtcgtt tcacagccaa gaattacaga attcaagtca gtctggtgtc 600
 tttgctaattg tgcagggaga atctcaaate gatgatgcaa ctacaccgat tgaggaggaa 660
 tggaaaacat ggttgaataa tgatggtgat gagcagagga atatcatgtt tatgcaagat 720
 catcgcagcg attacacacc tctaaagtcg ttaactggtg tcttcagtga tgatagcagt 780
 gatgataatg attctgattt gatattctct aaaacaaatt ctattggaac ttcgagcact 840
 tgtgctagtt ttgctagctc aaatcatcag atagacccaa ctcaacattc tcctgactca 900
 acagtccagc tagtgtcatt aactcaagag gtgagccaag gtccgggtca agtgactgtg 960
 attcgagagc ataaattggg tgaagagtct gtcaagaaga aaagagctag tttcgtttac 1020
 aggatgatac acagattagt caagaaaatt caccaatggt attctatctc aagaacatga 1080

<210> 24
 <211> 359
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> G517 polypeptide Paralogous to G2053

<400> 24

Met Met Asn Pro Val Gly Phe Arg Phe Arg Pro Asn Asp Glu Glu Ile
 1 5 10 15

Val Asp His Tyr Leu Arg Pro Lys Asn Leu Asp Ser Asp Thr Ser His
 20 25 30

MBI0058CIP.ST25.txt

Val	Asp	Glu	Val	Ile	Ser	Thr	Val	Asp	Ile	Cys	Ser	Phe	Glu	Pro	Trp	35	40	45	
Asp	Leu	Pro	Ser	Lys	Ser	Met	Ile	Lys	Ser	Arg	Asp	Gly	Val	Trp	Tyr	50	55	60	
Phe	Phe	Ser	Val	Lys	Glu	Met	Lys	Tyr	Asn	Arg	Gly	Asp	Gln	Gln	Arg	65	70	75	80
Arg	Arg	Thr	Asn	Ser	Gly	Phe	Trp	Lys	Lys	Thr	Gly	Lys	Thr	Met	Thr	85	90	95	
Val	Met	Arg	Lys	Arg	Gly	Asn	Arg	Glu	Lys	Ile	Gly	Glu	Lys	Arg	Val	100	105	110	
Leu	Val	Phe	Lys	Asn	Arg	Asp	Gly	Ser	Lys	Thr	Asp	Trp	Val	Met	His	115	120	125	
Glu	Tyr	His	Ala	Thr	Ser	Leu	Phe	Pro	Asn	Gln	Met	Met	Thr	Tyr	Thr	130	135	140	
Val	Cys	Lys	Val	Glu	Phe	Lys	Gly	Glu	Glu	Thr	Glu	Ile	Ser	Ser	Ser	145	150	155	160
Ser	Thr	Gly	Ser	Glu	Ile	Glu	Gln	Ile	His	Ser	Leu	Ile	Pro	Leu	Val	165	170	175	
Asn	Ser	Ser	Gly	Gly	Ser	Glu	Gly	Ser	Ser	Phe	His	Ser	Gln	Glu	Leu	180	185	190	
Gln	Asn	Ser	Ser	Gln	Ser	Gly	Val	Phe	Ala	Asn	Val	Gln	Gly	Glu	Ser	195	200	205	
Gln	Ile	Asp	Asp	Ala	Thr	Thr	Pro	Ile	Glu	Glu	Glu	Trp	Lys	Thr	Trp	210	215	220	
Leu	Asn	Asn	Asp	Gly	Asp	Glu	Gln	Arg	Asn	Ile	Met	Phe	Met	Gln	Asp	225	230	235	240
His	Arg	Ser	Asp	Tyr	Thr	Pro	Leu	Lys	Ser	Leu	Thr	Gly	Val	Phe	Ser	245	250	255	
Asp	Asp	Ser	Ser	Asp	Asp	Asn	Asp	Ser	Asp	Leu	Ile	Ser	Pro	Lys	Thr	260	265	270	
Asn	Ser	Ile	Gly	Thr	Ser	Ser	Thr	Cys	Ala	Ser	Phe	Ala	Ser	Ser	Asn	275	280	285	

MBI0058CIP.ST25.txt

His Gln Ile Asp Gln Thr Gln His Ser Pro Asp Ser Thr Val Gln Leu
290 295 300

Val Ser Leu Thr Gln Glu Val Ser Gln Gly Pro Gly Gln Val Thr Val
305 310 315 320

Ile Arg Glu His Lys Leu Gly Glu Glu Ser Val Lys Lys Lys Arg Ala
325 330 335

Ser Phe Val Tyr Arg Met Ile His Arg Leu Val Lys Lys Ile His Gln
340 345 350

Cys Tyr Ser Ile Ser Arg Thr
355

<210> 25
<211> 1413
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G592 Predicted polypeptide sequence is paralogous to G3086

<400> 25
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ttacaagaag agaaaacaga ggaaatttcg ttgcattttt ttacatatt gattcgatta 120
atggattcaa ataatcatct ctacgaccgc aatcccaccg ggtcgggtct tcttcgtttt 180
agatcagctc cgagctctgt tctcgccgct tttgttgacg acgacaagat tggtttcgac 240
tccgatagggt tgctttcaag attcgtgacc tctaattggcg ttaacggaga tctgggttca 300
cctaaattcg aggataagtc tccggtttcg ttaacgaaca cctctgtttc atacgccgcc 360
actctgccgc caccgccgca gcttgagccg tcgagttttc tgggtttgcc gccgcattac 420
ccgaggcaga gtaaagggat aatgaactcg gttggtttgg atcagtttct cggtatcaat 480
aatcatcaca ccaaaccagt tgaatctaatt cttctccgct aaagcagctc tccagccgga 540
atgtttacta atctctctga ccaaaacggt tatggttcaa tgaggaattt gatgaattac 600
gaagaagatg aagagagtcc atctaattcc aatggattaa gacgccattg cagtctctct 660
tcaaggccac cttcttcact tggaatgctt tctcaaatac ctgaaatcgc acccgaaact 720
aattttccat atagccattg gaatgatcca tccagcttta ttgataactt atcctcactt 780
aaaagagaag ccgaggacga tggaaaattg tttctcggag ctcagaacgg agagtccggg 840
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gacatgggtt cagtggataa gtatcttcag ctacaagatt ctgttccttg taaaatcaga 960
gccaaacgtg gttgcgctac acatcctcga agcatcgctg aacgggtaag aagaacgcgg 1020

MBI0058CIP.ST25.txt

ataagcgagc gaatgaggaa gttacaagag cttgttccta acatggacaa gcaaaccaac 1080
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attttaaacg acaacagagc taactgtaag tgtatgaaca aggagaagaa gtcaatatag 1200
ggcgcaacaa agtgtgtagt agataggact aaaaagcagg gagaaggaca agaaagaaac 1260
aatgtcatgt ctgaatattt tttagccgaa acagacccaa ttgtctatgt aagctctcga 1320
gaaaagcatc tgcttccaac aaaattctaa gtaataaaat agtactcgat ttgttcttat 1380
ttcattatta caatgcagaa tctactaatc aaa 1413

<210> 26

<211> 359

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G592 polypeptide Paralogous to G3086

<400> 26

Met Asp Ser Asn Asn His Leu Tyr Asp Pro Asn Pro Thr Gly Ser Gly
1 5 10 15

Leu Leu Arg Phe Arg Ser Ala Pro Ser Ser Val Leu Ala Ala Phe Val
20 25 30

Asp Asp Asp Lys Ile Gly Phe Asp Ser Asp Arg Leu Leu Ser Arg Phe
35 40 45

Val Thr Ser Asn Gly Val Asn Gly Asp Leu Gly Ser Pro Lys Phe Glu
50 55 60

Asp Lys Ser Pro Val Ser Leu Thr Asn Thr Ser Val Ser Tyr Ala Ala
65 70 75 80

Thr Leu Pro Pro Pro Pro Gln Leu Glu Pro Ser Ser Phe Leu Gly Leu
85 90 95

Pro Pro His Tyr Pro Arg Gln Ser Lys Gly Ile Met Asn Ser Val Gly
100 105 110

Leu Asp Gln Phe Leu Gly Ile Asn Asn His His Thr Lys Pro Val Glu
115 120 125

Ser Asn Leu Leu Arg Gln Ser Ser Ser Pro Ala Gly Met Phe Thr Asn
130 135 140

Leu Ser Asp Gln Asn Gly Tyr Gly Ser Met Arg Asn Leu Met Asn Tyr
145 150 155 160

Glu Glu Asp Glu Glu Ser Pro Ser Asn Ser Asn Gly Leu Arg Arg His
165 170 175

Cys Ser Leu Ser Ser Arg Pro Pro Ser Ser Leu Gly Met Leu Ser Gln
180 185 190

Ile Pro Glu Ile Ala Pro Glu Thr Asn Phe Pro Tyr Ser His Trp Asn
195 200 205

Asp Pro Ser Ser Phe Ile Asp Asn Leu Ser Ser Leu Lys Arg Glu Ala
210 215 220

Glu Asp Asp Gly Lys Leu Phe Leu Gly Ala Gln Asn Gly Glu Ser Gly
225 230 235 240

Asn Arg Met Gln Leu Leu Ser His His Leu Ser Leu Pro Lys Ser Ser
245 250 255

Ser Thr Ala Ser Asp Met Val Ser Val Asp Lys Tyr Leu Gln Leu Gln
260 265 270

Asp Ser Val Pro Cys Lys Ile Arg Ala Lys Arg Gly Cys Ala Thr His
275 280 285

Pro Arg Ser Ile Ala Glu Arg Val Arg Arg Thr Arg Ile Ser Glu Arg
290 295 300

Met Arg Lys Leu Gln Glu Leu Val Pro Asn Met Asp Lys Gln Thr Asn
305 310 315 320

Thr Ser Asp Met Leu Asp Leu Ala Val Asp Tyr Ile Lys Asp Leu Gln
325 330 335

Arg Gln Tyr Lys Ile Leu Asn Asp Asn Arg Ala Asn Cys Lys Cys Met
340 345 350

Asn Lys Glu Lys Lys Ser Ile
355

<210> 27

<211> 1064

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G1134 Predicted polypeptide sequence is paralogous to G3086

<400> 27

taaagaaaga gaaaaaaagc tttcgtagtg tctattgaaa ccagagaaaa gccaaagggg

60

MBI0058CIP.ST25.txt

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atgcaaccaa catccgtcgg tagtagcggc ggtggtgacg acggaggagg cagaggagga 120
ggaggagggc taagtagaag tggactatct cggatccgtt cagctccagc gacttggtt 180
gaagctttac ttgaggaaga tgaagaagag tctttgaaac ctaatcttgg tctcaccgat 240
ttgcttaccg ggaactcgaa cgatttaccg acaagtcgcg gctcgttcga gttcccgtt 300
cctgttgagc aagggttgta tcaacaaggt gggtttcacc gacagaatag tactccggcg 360
gattttctta gtggttctga tggatttatc caaagctttg ggattcaggc gaattacgat 420
tacttatcgg ggaatatcga tgtttctccg ggaagtaagc ggtctagaga aatggaagca 480
ctcttctctt ctcttgagtt tactttctcaa atgaaaggag agcaaagcag cggtaagtt 540
cctaccggag tatcaagcat gtcggatatg aacatggaga accttatgga ggactctgtt 600
gcttttaggg ttcgggctaa acgtgggtgc gcaactcatc cccgcagcat tgccgagagg 660
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<210> 28

<211> 262

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G1134 polypeptide Paralogous to G3086

<400> 28

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Met Gln Pro Thr Ser Val Gly Ser Ser Gly Gly Gly Asp Asp Gly Gly
1           5           10          15

```

```

Gly Arg Gly Gly Gly Gly Gly Leu Ser Arg Ser Gly Leu Ser Arg Ile
          20          25          30

```

```

Arg Ser Ala Pro Ala Thr Trp Leu Glu Ala Leu Leu Glu Glu Asp Glu
          35          40          45

```

```

Glu Glu Ser Leu Lys Pro Asn Leu Gly Leu Thr Asp Leu Leu Thr Gly
          50          55          60

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```

Asn Ser Asn Asp Leu Pro Thr Ser Arg Gly Ser Phe Glu Phe Pro Ile
65          70          75          80

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MBI0058CIP.ST25.txt

Pro Val Glu Gln Gly Leu Tyr Gln Gln Gly Gly Phe His Arg Gln Asn
85 90 95

Ser Thr Pro Ala Asp Phe Leu Ser Gly Ser Asp Gly Phe Ile Gln Ser
100 105 110

Phe Gly Ile Gln Ala Asn Tyr Asp Tyr Leu Ser Gly Asn Ile Asp Val
115 120 125

Ser Pro Gly Ser Lys Arg Ser Arg Glu Met Glu Ala Leu Phe Ser Ser
130 135 140

Pro Glu Phe Thr Ser Gln Met Lys Gly Glu Gln Ser Ser Gly Gln Val
145 150 155 160

Pro Thr Gly Val Ser Ser Met Ser Asp Met Asn Met Glu Asn Leu Met
165 170 175

Glu Asp Ser Val Ala Phe Arg Val Arg Ala Lys Arg Gly Cys Ala Thr
180 185 190

His Pro Arg Ser Ile Ala Glu Arg Val Arg Arg Thr Arg Ile Ser Asp
195 200 205

Arg Ile Arg Lys Leu Gln Glu Leu Val Pro Asn Met Asp Lys Gln Thr
210 215 220

Asn Thr Ala Asp Met Leu Glu Glu Ala Val Glu Tyr Val Lys Val Leu
225 230 235 240

Gln Arg Gln Ile Gln Glu Leu Thr Glu Glu Gln Lys Arg Cys Thr Cys
245 250 255

Ile Pro Lys Glu Glu Gln
260

<210> 29

<211> 748

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G1275 Predicted polypeptide sequence is paralogous to G1274

<400> 29

ccaagaaaag ggaagatcac gcattcttat aggcgtaatt cgtaaatagt ggtgagtatg 60

aatgatgcag acacaaactt ggggagtagt ttcagcgatg atactcactc tgtgttcgag 120

tttccggagc tagacttgtc agatgaatgg atggatgatg atcttggtgc tgcggtttcc 180

MBI0058CIP.ST25.txt

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gggatgaatc agtcttatgg ttatcagact agtgatgttg ctgggtgcttt attctcaggt      240
tcttctagct gtttcagtca tcttgaatct ccaagtagca aaacttatgt tgctgctaca      300
gccactgctt ctgccgacaa ccaaaacaag aaagaaaaga aaaaaattaa agggagagtt      360
gcgttcaaga cacggtccga ggtggaagtg cttgacgacg ggttcaagtg gagaaagtat      420
gggaagaaga tggatgaaga cagcccat ccaagaaact actacaaatg ttcagttgat      480
ggctgtcccg tgaagaaaag ggttgaacga gacagagatg atccgagctt tgtgataaca      540
acttacgagg gttcccacaa tcaactcaagc atgaactaag actcgaacta aggctcaagg      600
cgaccatgct atattcagca catcttattt tctatgggta cgaacgatac ttaaaactgc      660
ttctagttct ttatatccat tgtaaactgg ttgcagggttc acaaattttg agaggtttat      720
gacattctaa atctgtagta cttatata                                          748

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<210> 30
 <211> 173
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> G1275 polypeptide Paralogous to G1274

<400> 30

Met Asn Asp Ala Asp Thr Asn Leu Gly Ser Ser Phe Ser Asp Asp Thr
 1 5 10 15

His Ser Val Phe Glu Phe Pro Glu Leu Asp Leu Ser Asp Glu Trp Met
 20 25 30

Asp Asp Asp Leu Val Ser Ala Val Ser Gly Met Asn Gln Ser Tyr Gly
 35 40 45

Tyr Gln Thr Ser Asp Val Ala Gly Ala Leu Phe Ser Gly Ser Ser Ser
 50 55 60

Cys Phe Ser His Pro Glu Ser Pro Ser Thr Lys Thr Tyr Val Ala Ala
 65 70 75 80

Thr Ala Thr Ala Ser Ala Asp Asn Gln Asn Lys Lys Glu Lys Lys Lys
 85 90 95

Ile Lys Gly Arg Val Ala Phe Lys Thr Arg Ser Glu Val Glu Val Leu
 100 105 110

Asp Asp Gly Phe Lys Trp Arg Lys Tyr Gly Lys Lys Met Val Lys Asn
 115 120 125

Ser Pro His Pro Arg Asn Tyr Tyr Lys Cys Ser Val Asp Gly Cys Pro

130

135

140

Val Lys Lys Arg Val Glu Arg Asp Arg Asp Asp Pro Ser Phe Val Ile
145 150 155 160

Thr Thr Tyr Glu Gly Ser His Asn His Ser Ser Met Asn
165 170

<210> 31
<211> 896
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G1758 Predicted polypeptide sequence is paralogous to G1274

<400> 31
gtccctcctc ttagcttcaa cgcgccgaaa aactaaacaa ccttcttgga aaaaaagaga 60
aactaaaaat gaactatcct tcaaacccta accctagctc cacagatttc actgaatttt 120
tcaagttcga tgattttgac gatacttttg agaagatcat ggaagaaatc ggccgtgagg 180
accactcgtc gtcaccgact ttgagttgga gttcatcgga aaagttagtg gctgcagaaa 240
tcacaagccc gcttcaaaca agcctagcta cctcacctat gagctttgaa ataggtgaca 300
aagatgaaat caaaaagagg aagagacaca aagaagatcc gattattcac gtcttcaaaa 360
cgaaatcatc aattgatgaa aagggttgctt tagatgatgg gtataaatgg aggaaatacg 420
gaaagaagcc gataacgggt agtccatttc caaggcatta tcacaagtgt tcgagcccag 480
attgcaacgt gaagaagaag atcgaaagag atacgaacaa tccagattac atattgacaa 540
catacgaagg tagacataac cacccaagcc cttctgtagt ttattgtgat tcagacgact 600
ttgatcttaa ctctctcaac aattggctct ttcagacggc aaatacgtat agtttctctc 660
attctgctcc atattgatcg atcgtagtta caagtttggtg tatatagatg tatatatata 720
tatcaccaat tcaccatcgt aatcacgtct cacatgtaac tacgtacata tatcttggtc 780
ggggttcggt ttgtaatgta ttgaattggt ggaggtagaa tggaagtcac cttgtatagt 840
tgtacttgta tgtaagggtt gatagtcatt ttttataaag taactaattt gtacaa 896

<210> 32
<211> 202
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G1758 polypeptide Paralogous to G1274

<400> 32

Met Asn Tyr Pro Ser Asn Pro Asn Pro Ser Ser Thr Asp Phe Thr Glu
1 5 10 15

MBI0058CIP.ST25.txt

Phe Phe Lys Phe Asp Asp Phe Asp Asp Thr Phe Glu Lys Ile Met Glu
20 25 30

Glu Ile Gly Arg Glu Asp His Ser Ser Ser Pro Thr Leu Ser Trp Ser
35 40 45

Ser Ser Glu Lys Leu Val Ala Ala Glu Ile Thr Ser Pro Leu Gln Thr
50 55 60

Ser Leu Ala Thr Ser Pro Met Ser Phe Glu Ile Gly Asp Lys Asp Glu
65 70 75 80

Ile Lys Lys Arg Lys Arg His Lys Glu Asp Pro Ile Ile His Val Phe
85 90 95

Lys Thr Lys Ser Ser Ile Asp Glu Lys Val Ala Leu Asp Asp Gly Tyr
100 105 110

Lys Trp Arg Lys Tyr Gly Lys Lys Pro Ile Thr Gly Ser Pro Phe Pro
115 120 125

Arg His Tyr His Lys Cys Ser Ser Pro Asp Cys Asn Val Lys Lys Lys
130 135 140

Ile Glu Arg Asp Thr Asn Asn Pro Asp Tyr Ile Leu Thr Thr Tyr Glu
145 150 155 160

Gly Arg His Asn His Pro Ser Pro Ser Val Val Tyr Cys Asp Ser Asp
165 170 175

Asp Phe Asp Leu Asn Ser Leu Asn Asn Trp Ser Phe Gln Thr Ala Asn
180 185 190

Thr Tyr Ser Phe Ser His Ser Ala Pro Tyr
195 200

<210> 33

<211> 549

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G1791 Predicted polypeptide sequence is paralogous to G1792

<400> 33

atgtacatgc aaaaacaaaa accttaaaag ctttcatgga acgtatagag tcttataaca 60

cgaatgagat gaaatacaga ggcgtacgaa agcgtccatg gggaaaatat gcggcggaga 120

ttcgcgactc agctagacac ggtgctcgtg tttggcttgg gacgtttaac acagcgggaag 180

MBI0058CIP.ST25.txt

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acgcggctcg ggcttatgat agagcagctt tcggcatgag aggccaaagg gccattctca 240
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tggttcctc gtcgtcggga tatagaggag gaggtggtgg tgatgatggg agggaagtta 360
ttgagttcga gtatttggat gatagtttat tggaggagct tttagattat ggtgagagat 420
ctaaccaaga caattgtaac gacgcaaacc gctagatcat cactacttac ttacagtgta 480
atgtttttgg agtaaagagt aataatcaat ataataact ttagtttagg aaaaaaaaaa 540
aaaaaaaaa 549
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<210> 34
 <211> 139
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> G1791 polypeptide Paralogous to G1792

<400> 34

Met Glu Arg Ile Glu Ser Tyr Asn Thr Asn Glu Met Lys Tyr Arg Gly
 1 5 10 15

Val Arg Lys Arg Pro Trp Gly Lys Tyr Ala Ala Glu Ile Arg Asp Ser
 20 25 30

Ala Arg His Gly Ala Arg Val Trp Leu Gly Thr Phe Asn Thr Ala Glu
 35 40 45

Asp Ala Ala Arg Ala Tyr Asp Arg Ala Ala Phe Gly Met Arg Gly Gln
 50 55 60

Arg Ala Ile Leu Asn Phe Pro His Glu Tyr Gln Met Met Lys Asp Gly
 65 70 75 80

Pro Asn Gly Ser His Glu Asn Ala Val Ala Ser Ser Ser Ser Gly Tyr
 85 90 95

Arg Gly Gly Gly Gly Gly Asp Asp Gly Arg Glu Val Ile Glu Phe Glu
 100 105 110

Tyr Leu Asp Asp Ser Leu Leu Glu Glu Leu Leu Asp Tyr Gly Glu Arg
 115 120 125

Ser Asn Gln Asp Asn Cys Asn Asp Ala Asn Arg
 130 135

<210> 35
 <211> 450
 <212> DNA

<213> Arabidopsis thaliana

<220>

<223> G1795 Predicted polypeptide sequence is paralogous to G1792

<400> 35

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acaaacacgc aaaaagtcac taatatatgg atcaaggagg tcgagggtgc ggtgccgagc      60
atggaaagta ccgggggagtt cggagacgac cttggggaaa atatgcagca gagatacgag      120
attcgaggaa gcacggtgaa cgtgtgtggc ttggaacggt cgatacggca gaggaagcgg      180
ctagagccta tgaccaagct gcttactcca tgagaggcca agcagcaatc cttaacttcc      240
ctcatgagta taacatgggg agtggtgtct cttcttccac cgccatggct ggatcttcct      300
ccgcctccgc ctccgcttct tcttcttcta ggcaagtttt tgaatttgag tacttggatg      360
atagtgtttt ggaggagctc cttgaggaag gagagaaacc taacaagggc aagaagaaat      420
gagcgagata taattcatga ttatttctaa      450

```

<210> 36

<211> 131

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G1795 polypeptide Paralogous to G1792

<400> 36

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Met Asp Gln Gly Gly Arg Gly Val Gly Ala Glu His Gly Lys Tyr Arg
1          5          10          15

Gly Val Arg Arg Arg Pro Trp Gly Lys Tyr Ala Ala Glu Ile Arg Asp
          20          25          30

Ser Arg Lys His Gly Glu Arg Val Trp Leu Gly Thr Phe Asp Thr Ala
          35          40          45

Glu Glu Ala Ala Arg Ala Tyr Asp Gln Ala Ala Tyr Ser Met Arg Gly
          50          55          60

Gln Ala Ala Ile Leu Asn Phe Pro His Glu Tyr Asn Met Gly Ser Gly
65          70          75          80

Val Ser Ser Ser Thr Ala Met Ala Gly Ser Ser Ser Ala Ser Ala Ser
          85          90          95

Ala Ser Ser Ser Ser Arg Gln Val Phe Glu Phe Glu Tyr Leu Asp Asp
          100          105          110

Ser Val Leu Glu Glu Leu Leu Glu Glu Gly Glu Lys Pro Asn Lys Gly
          115          120          125

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Lys Lys Lys
130

<210> 37
<211> 1353
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G2149 Predicted polypeptide sequence is paralogous to G3086

<400> 37
aatcttttat ttttctttta gaaaccaaac ttttcagatt tctctctctc catttggcga 60
tagaagaagt catgtaccaa tcatcatcct ccacgtcatc atcatcgcag agatcatcgc 120
ttccccggcgg cggaggactg atccgttacg gctcagctcc gggatcggtt cttaaactctg 180
tggttgacga agtcatcggg ggaggtcatc caaacgctcg tgacttcacc ggctatcaac 240
cgtcgtcgga taacttcacg ggtaactttt tcaccggagc tgctgactca tcctcgctga 300
gatccgattc gacgacttgt ggagtcaaca actcatccga cggacagaaa cagctaggca 360
ataacaataa taataatagt aataaagata tcttcctcga cagatcctac ggtggattca 420
acgagatctc gcaacaacac aagagcaacg acatcggagg aggaaacagc tcaggatctt 480
actctctcgc tagacaacgt agctctcccg ccgattttctt cacctacctc gcctcagata 540
aaaacaattt ctcggtgaac caaccaacca gtgattatag tccgcaagga gggctctaatg 600
ggggacgagg acattccaga ttgaagtctc agctaagctt cacgaatcac gactctctgg 660
ctcggatcaa cgagggtcaat gagaccccag tccacgacgg ttcaggccat tcgttttctg 720
cggctagctt tgggtgcagc actactgatt cttgggatga cggttccggt tcgatagggt 780
ttaccgtgac taggcccagt aaacgatcca aggacatgga ctctggtctc ttttcgcagt 840
atagtcttcc ttcagacact tcaatgaact acatggataa cttcatgcag cttccagaag 900
attctgtacc ctgcaaaatc cgggccaac gcggtgctc caccatcct agaagcatcg 960
ctgagcggga gaggagaacg agaataagtg ggaagctaaa gaagctacaa gatcttgtcc 1020
ccaacatgga taagcaaaca agctattcag acatgctgga tttagctgta caacacatca 1080
aaggccttca gcatcaactt cagaatttga aaaaagatca agagaattgc acgtgtgggt 1140
gcagtgagaa accaagctag ctcaaacca aaggtagggg catcctaatt ttatttgcac 1200
tgttccgatt ttatcatatg agagaattag agaagatgta aataaaatag attatattaa 1260
atgtctaata ctcttataat taagctctc attcgttatc attataagat agaacagtga 1320
caattgtcca ttatgttttt gtttcaagtt tat 1353

<210> 38
<211> 362
<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G2149 polypeptide Paralogous to G3086

<400> 38

Met Tyr Gln Ser Ser Ser Ser Thr Ser Ser Ser Ser Gln Arg Ser Ser
1 5 10 15

Leu Pro Gly Gly Gly Gly Leu Ile Arg Tyr Gly Ser Ala Pro Gly Ser
20 25 30

Phe Leu Asn Ser Val Val Asp Glu Val Ile Gly Gly Gly Ser Ser Asn
35 40 45

Ala Arg Asp Phe Thr Gly Tyr Gln Pro Ser Ser Asp Asn Phe Ile Gly
50 55 60

Asn Phe Phe Thr Gly Ala Ala Asp Ser Ser Ser Leu Arg Ser Asp Ser
65 70 75 80

Thr Thr Cys Gly Val Asn Asn Ser Ser Asp Gly Gln Lys Gln Leu Gly
85 90 95

Asn Asn Asn Asn Asn Asn Ser Asn Lys Asp Ile Phe Leu Asp Arg Ser
100 105 110

Tyr Gly Gly Phe Asn Glu Ile Ser Gln Gln His Lys Ser Asn Asp Ile
115 120 125

Gly Gly Gly Asn Ser Ser Gly Ser Tyr Ser Leu Ala Arg Gln Arg Ser
130 135 140

Ser Pro Ala Asp Phe Phe Thr Tyr Leu Ala Ser Asp Lys Asn Asn Phe
145 150 155 160

Ser Leu Asn Gln Pro Thr Ser Asp Tyr Ser Pro Gln Gly Gly Ser Asn
165 170 175

Gly Gly Arg Gly His Ser Arg Leu Lys Ser Gln Leu Ser Phe Thr Asn
180 185 190

His Asp Ser Leu Ala Arg Ile Asn Glu Val Asn Glu Thr Pro Val His
195 200 205

Asp Gly Ser Gly His Ser Phe Ser Ala Ala Ser Phe Gly Ala Ala Thr
210 215 220

Thr Asp Ser Trp Asp Asp Gly Ser Gly Ser Ile Gly Phe Thr Val Thr

225 230 235 240

Arg Pro Ser Lys Arg Ser Lys Asp Met Asp Ser Gly Leu Phe Ser Gln
245 250 255

Tyr Ser Leu Pro Ser Asp Thr Ser Met Asn Tyr Met Asp Asn Phe Met
260 265 270

Gln Leu Pro Glu Asp Ser Val Pro Cys Lys Ile Arg Ala Lys Arg Gly
275 280 285

Cys Ala Thr His Pro Arg Ser Ile Ala Glu Arg Glu Arg Arg Thr Arg
290 295 300

Ile Ser Gly Lys Leu Lys Lys Leu Gln Asp Leu Val Pro Asn Met Asp
305 310 315 320

Lys Gln Thr Ser Tyr Ser Asp Met Leu Asp Leu Ala Val Gln His Ile
325 330 335

Lys Gly Leu Gln His Gln Leu Gln Asn Leu Lys Lys Asp Gln Glu Asn
340 345 350

Cys Thr Cys Gly Cys Ser Glu Lys Pro Ser
355 360

<210> 39

<211> 1167

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G2555 Predicted polypeptide sequence is paralogous to G3086

<400> 39

ctgttttttgt atccgtgtaa attaatacaca cggtagtttt tgatgaaaag acaacaatcg 60

gagaacaatc tgggtctgctg ctaaaattta ataaattggt ttgtctaatt gtctccaccc 120

ataaaaaagc gcgaattcaa ttcaccgact aaagacattc tccggtggag accccgatgc 180

aatccactca tataagcggc ggaagtagcg gtggtggtgg tggaggagga ggagaggtga 240

gtcgaagtgg attatctcgg atccgttcag ctccagctac ttggattgaa accctactcg 300

aagaagatga agaagaaggt ttaaaaccta acctttgttt aacagagctg cttactggtga 360

ataataactc tggaggagtg ataacgagtc gtgacgactc gttcgagttc ctgagttctg 420

ttgagcaagg attgtataat catcatcaag gtggtggctt tcaccgtcag aatagttctc 480

cggtctgattt tcttagtggg tctggttctg ggactgatgg gtatttctct aattttggta 540

ttccggcgaa ttatgactat ttgtcgacca acgttgatat ttctccgact aaacggtcta 600

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caggaatgat ggatatgaac atggacaaga tttttgagga ttcagttcct tgtagggttc 720
gtgctaaacg tggttgtgct actcatcctc gtagcattgc tgaacgggtg agaagaacgc 780
gaataagtga tcggattagg aggctgcaag agcttggtcc taacatggat aagcaaacca 840
aactgcaga catgttgga gaagctgtgg agtatgtgaa ggctcttcaa agccagatcc 900
aggaattgac agagcagcag aagagatgca aatgcaaacc taaagaagaa caataatgta 960
tccttttagga tttgatatat ctgtatttta tttttgtact atctaataat ggtgatgatc 1020
tgttcgaaaa ttcgaaacat gatcttatat attgaactag aaaaaataga tatatatgaa 1080
ttttagctgt aaaatttttg tacaataagg agaaaaagat ttagaagagt caataaaaag 1140
atgatgttta caagtcaaaa aaaaaaa 1167

<210> 40

<211> 259

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G2555 polypeptide Paralogous to G3086

<400> 40

Met Gln Ser Thr His Ile Ser Gly Gly Ser Ser Gly Gly Gly Gly Gly
1 5 10 15

Gly Gly Gly Glu Val Ser Arg Ser Gly Leu Ser Arg Ile Arg Ser Ala
20 25 30

Pro Ala Thr Trp Ile Glu Thr Leu Leu Glu Glu Asp Glu Glu Glu Gly
35 40 45

Leu Lys Pro Asn Leu Cys Leu Thr Glu Leu Leu Thr Gly Asn Asn Asn
50 55 60

Ser Gly Gly Val Ile Thr Ser Arg Asp Asp Ser Phe Glu Phe Leu Ser
65 70 75 80

Ser Val Glu Gln Gly Leu Tyr Asn His His Gln Gly Gly Gly Phe His
85 90 95

Arg Gln Asn Ser Ser Pro Ala Asp Phe Leu Ser Gly Ser Gly Ser Gly
100 105 110

Thr Asp Gly Tyr Phe Ser Asn Phe Gly Ile Pro Ala Asn Tyr Asp Tyr
115 120 125

Leu Ser Thr Asn Val Asp Ile Ser Pro Thr Lys Arg Ser Arg Asp Met

130 135 140

Glu Thr Gln Phe Ser Ser Gln Leu Lys Glu Glu Gln Met Ser Gly Gly
 145 150 155 160

Ile Ser Gly Met Met Asp Met Asn Met Asp Lys Ile Phe Glu Asp Ser
 165 170 175

Val Pro Cys Arg Val Arg Ala Lys Arg Gly Cys Ala Thr His Pro Arg
 180 185 190

Ser Ile Ala Glu Arg Val Arg Arg Thr Arg Ile Ser Asp Arg Ile Arg
 195 200 205

Arg Leu Gln Glu Leu Val Pro Asn Met Asp Lys Gln Thr Asn Thr Ala
 210 215 220

Asp Met Leu Glu Glu Ala Val Glu Tyr Val Lys Ala Leu Gln Ser Gln
 225 230 235 240

Ile Gln Glu Leu Thr Glu Gln Gln Lys Arg Cys Lys Cys Lys Pro Lys
 245 250 255

Glu Glu Gln

<210> 41
 <211> 1304
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <223> G2766 Predicted polypeptide sequence is paralogous to G3086

<400> 41
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 ggcggcgatg ccgacaccaa tcaatatgac tcagccgctg gagctaccgc tgatttctcc 180
 tctcttgggc ctcaaaccce ccatcatccg ccaccgcagc ggcagcagca gcatcagcag 240
 aatcccaacc tcgtcggcca ttatttaccg ggcgagccat cttccatcgg attcgattcc 300
 aacgcttctt cttcgtcttc tttgttcgca cacagaagct ctccggctgg attctacgac 360
 caacatcttc cactgatcc caacggtttt tctctaggac ggccaaacgg aggctacggc 420
 ggaggaggag agcaagggcc gtcgaggttg aagtcggagc tgagattctc tagtgggagt 480
 agtagccatc aagaacataa ttctctaccg cgaatctcgg aggttgaagc ggctgcagcg 540
 gctagaaacg gtgtcgcac cagtagtatg agttttggaa ataatcgtac taacaattgg 600

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 acaatggaga acttgatgaa catcccagag gactcgggtgc cttgtagggc tagagccaag 780
 cgcggtcttcg cgactcacc acgcagcatt gctgaaaggg agagaagaac gaggataagc 840
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 tcgatcaatc gatttttttt ttctgtttt cctcaaagtt ggtaatttt agcttagagc 1260
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<210> 42

<211> 309

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G2766 polypeptide Paralogous to G3086

<400> 42

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Asp Ala Asp Thr Asn Gln Tyr Asp Ser Ala Ala Gly Ala Thr Arg Asp
 20 25 30

Phe Ser Ser Leu Gly Pro Gln Thr His His His Pro Pro Pro Gln Arg
 35 40 45

Gln Gln Gln His Gln Gln Asn Pro Asn Leu Val Gly His Tyr Leu Pro
 50 55 60

Gly Glu Pro Ser Ser Ile Gly Phe Asp Ser Asn Ala Ser Ser Ser Ser
 65 70 75 80

Ser Leu Phe Arg His Arg Ser Ser Pro Ala Gly Phe Tyr Asp Gln His
 85 90 95

Leu Pro Thr Asp Pro Asn Gly Phe Ser Leu Gly Arg Pro Asn Gly Gly
 100 105 110

Tyr Gly Gly Gly Gly Glu Gln Gly Pro Ser Arg Leu Lys Ser Glu Leu

115

120

125

Arg Phe Ser Ser Gly Ser Ser Ser His Gln Glu His Asn Ser Leu Pro
130 135 140

Arg Ile Ser Glu Val Glu Ala Ala Ala Ala Ala Arg Asn Gly Val Ala
145 150 155 160

Ser Ser Ser Met Ser Phe Gly Asn Asn Arg Thr Asn Asn Trp Asp Asn
165 170 175

Ser Ser Ser His Ile Ser Phe Thr Ile Asp Gln Pro Gly Lys Arg Ser
180 185 190

Lys Asn Ser Asp Phe Phe Thr Leu Glu Thr Gln Tyr Ser Met Pro Gln
195 200 205

Thr Thr Leu Glu Met Ala Thr Met Glu Asn Leu Met Asn Ile Pro Glu
210 215 220

Asp Ser Val Pro Cys Arg Ala Arg Ala Lys Arg Gly Phe Ala Thr His
225 230 235 240

Pro Arg Ser Ile Ala Glu Arg Glu Arg Arg Thr Arg Ile Ser Gly Lys
245 250 255

Leu Lys Lys Leu Gln Glu Leu Val Pro Asn Met Asp Lys Gln Thr Ser
260 265 270

Tyr Ala Asp Met Leu Asp Leu Ala Val Glu His Ile Lys Gly Leu Gln
275 280 285

His Gln Val Glu Ser Leu Glu Lys Gly Met Glu Arg Cys Thr Cys Gly
290 295 300

Ala Cys Lys Lys Arg
305

<210> 43
<211> 1011
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G2989 Predicted polypeptide sequence is paralogous to G2999

<400> 43
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atgcttgaag ttagatcaat ggatatgact ccaaaatcac cagaacccga atccgaaact 120

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cgcacccgga tccaaccagc taaaccaatc tctttcagta acggaatcat caaacgccac 180
caccaccacc accacaacaa caacaaagtc acttaciaag aatgtctcaa gaaccacgcg 240
gcggcgattg gtggtcacgc gcttgacggg tgccggcgaat ttatgccgtc tccttcgtca 300
acaccttccg atccaacttc tctcaagtgt gcagcttggtg gttgtcaccg taacttccac 360
cgccgtgaaa ctgacgattc ctccgccggt ccaccaccgt ctcttcttcc atcttcaaca 420
acaaccgccg caattgagta tcagcctcat caccgtcatc atcctcctcc tccgctagct 480
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tcaaatcaga aagagaagat gcatgaattc gccgatcgaa tcggttggaa gattcagaaa 720
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<210> 44
 <211> 312
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> G2989 polypeptide Paralogous to G2999
 <400> 44

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 1 5 10 15

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 20 25 30

Ser Asn Gly Ile Ile Lys Arg His His His His His His Asn Asn Asn
 35 40 45

Lys Val Thr Tyr Lys Glu Cys Leu Lys Asn His Ala Ala Ala Ile Gly
 50 55 60

Gly His Ala Leu Asp Gly Cys Gly Glu Phe Met Pro Ser Pro Ser Ser
 65 70 75 80

Thr Pro Ser Asp Pro Thr Ser Leu Lys Cys Ala Ala Cys Gly Cys His
 85 90 95

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Arg Asn Phe His Arg Arg Glu Thr Asp Asp Ser Ser Ala Val Pro Pro
100 105 110

Pro Ser Leu Leu Pro Ser Ser Thr Thr Thr Ala Ala Ile Glu Tyr Gln
115 120 125

Pro His His Arg His His Pro Pro Pro Pro Leu Ala Pro Pro Leu Pro
130 135 140

Arg Ser Pro Asn Ser Ser Ser Pro Pro Pro Ile Ser Ser Ser Tyr Met
145 150 155 160

Leu Leu Ala Leu Ser Gly Asn Asn Lys Thr Ala Pro Phe Ser Asp Leu
165 170 175

Asn Phe Ala Ala Ala Ala Asn His Leu Ser Ala Thr Pro Gly Ser Arg
180 185 190

Lys Arg Phe Arg Thr Lys Phe Ser Ser Asn Gln Lys Glu Lys Met His
195 200 205

Glu Phe Ala Asp Arg Ile Gly Trp Lys Ile Gln Lys Arg Asp Glu Asp
210 215 220

Glu Val Arg Asp Phe Cys Arg Glu Ile Gly Val Asp Lys Gly Val Leu
225 230 235 240

Lys Val Trp Met His Asn Asn Lys Asn Ser Phe Lys Phe Ser Gly Gly
245 250 255

Gly Ala Thr Thr Val Gln Arg Asn Asp Asn Gly Ile Gly Gly Glu Asn
260 265 270

Ser Asn Asp Asp Gly Val Arg Gly Leu Ala Asn Asp Gly Asp Gly Gly
275 280 285

Gly Gly Arg Phe Glu Ser Asp Ser Gly Gly Ala Asp Gly Gly Gly Asn
290 295 300

Val Asn Ala Ser Ser Ser Ser Ser
305 310

<210> 45

<211> 1107

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G2990 Predicted polypeptide sequence is paralogous to G2999


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<400> 45
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tctacaata acaacaaca caacaccaac tctaaatca cccgaaccgg aatccgaaac      120
tccgaccggg atccaaccgg cgaaacccat ttccttttagc aacggcatca tcaaacgcca      180
ccaccaccac caccatcctc tcctcttttac ttacaaagaa tgtctcaaaa accacgcggc      240
ggcttttaggt ggtcacgctc tcgacgggtg cggcgaattc atgccgtctc cgtcgtcaat      300
ctcctccgat ccaacttctc tcaaagtgtg tgcttgtggc tgccaccgta atttccaccg      360
ccgtgatcca gataacaaca acgactcttc ccaaatecct cctcctcctt ccaccgccgt      420
agagtatcaa cctcaccacc gtcattcatc accaccacca ccacctcctc caccaccacg      480
tagtcctaac tcagcttctc ctccaccaat ctcttctctt tacatgctct tatctctctc      540
cggctactaat aacaacaaca acaacttagc ttctttctcc gatcttaact tctccgccgg      600
aaacaaccac caccaccacc accaacatac tcttcacgga tctcgtaaaa gattccgaac      660
aaaattcagc cagtttcaga aagagaagat gcatgaattc gccgaacgtg ttggttgga      720
gatgcaaaaa cgtgacgaag acgatgttcg tgatttttgc cggcagatcg gagttgataa      780
aagtgttctc aaagtttgga tgcataacaa caaaaacacc tttaaccgcc gtgatatcgc      840
cggaaacgag atccggcaaa tcgataacgg cggaggaaac cacactccga ttctcgccgg      900
cgagattaat aaccataaca atggacacca cgggtgtcggg ggaggaggag agcttcacca      960
gagtgttagt agcggcgggt gtggcggagg atttgatagt gatagcggcg gagctaacgg     1020
tggtaacgtt aacggatcat cgtcgtcgtg aagttaaaga tgagagtgtc aggttaataa     1080
gaagcttaga gtaagcttat tcggata                                         1107

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<210> 46
<211> 334
<212> PRT
<213> Arabidopsis thaliana

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<220>
<223> G2990 polypeptide Paralogous to G2999

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<400> 46

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1          5          10          15

```

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Lys Ser Pro Glu Pro Glu Ser Glu Thr Pro Thr Arg Ile Gln Pro Ala
20          25          30

```

```

Lys Pro Ile Ser Phe Ser Asn Gly Ile Ile Lys Arg His His His His
35          40          45

```

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His His Pro Leu Leu Phe Thr Tyr Lys Glu Cys Leu Lys Asn His Ala
Page 45

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50 55 60

Ala Ala Leu Gly Gly His Ala Leu Asp Gly Cys Gly Glu Phe Met Pro
65 70 75 80

Ser Pro Ser Ser Ile Ser Ser Asp Pro Thr Ser Leu Lys Cys Ala Ala
85 90 95

Cys Gly Cys His Arg Asn Phe His Arg Arg Asp Pro Asp Asn Asn Asn
100 105 110

Asp Ser Ser Gln Ile Pro Pro Pro Pro Ser Thr Ala Val Glu Tyr Gln
115 120 125

Pro His His Arg His His Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro
130 135 140

Arg Ser Pro Asn Ser Ala Ser Pro Pro Pro Ile Ser Ser Ser Tyr Met
145 150 155 160

Leu Leu Ser Leu Ser Gly Thr Asn Asn Asn Asn Asn Asn Leu Ala Ser
165 170 175

Phe Ser Asp Leu Asn Phe Ser Ala Gly Asn Asn His His His His His
180 185 190

Gln His Thr Leu His Gly Ser Arg Lys Arg Phe Arg Thr Lys Phe Ser
195 200 205

Gln Phe Gln Lys Glu Lys Met His Glu Phe Ala Glu Arg Val Gly Trp
210 215 220

Lys Met Gln Lys Arg Asp Glu Asp Asp Val Arg Asp Phe Cys Arg Gln
225 230 235 240

Ile Gly Val Asp Lys Ser Val Leu Lys Val Trp Met His Asn Asn Lys
245 250 255

Asn Thr Phe Asn Arg Arg Asp Ile Ala Gly Asn Glu Ile Arg Gln Ile
260 265 270

Asp Asn Gly Gly Gly Asn His Thr Pro Ile Leu Ala Gly Glu Ile Asn
275 280 285

Asn His Asn Asn Gly His His Gly Val Gly Gly Gly Gly Glu Leu His
290 295 300

Gln Ser Val Ser Ser Gly Gly Gly Gly Gly Gly Phe Asp Ser Asp Ser

305

310

315

320

Gly Gly Ala Asn Gly Gly Asn Val Asn Gly Ser Ser Ser Ser
325 330

<210> 47

<211> 914

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G2991 Predicted polypeptide sequence is paralogous to G2999

<400> 47

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cgaagctccg atccggatcc agcccgcgaa gcctattttct ttctcaaacg gcaaacgctg      180
ccaccaccat catcttgcat ctgaagcggg tgcgggtgcg acttataaag aatgtctaaa      240
gaatcacgca gcaggtatcg gcggtcacgc tttagacgga tgcggcgagt ttatgccgtc      300
accgtcgttt aactccaatg accccgcttc actaacgtgc gctgcttggt gttgccaccg      360
taacttccac cgccgtgagg aggatccatc ttctctctct gccatcgtcc ctgcatcga      420
atttcgacct cacaaccgtc accagcttcc tccaccgcct cctcctcatc tggcggggat      480
tcgtagtcca gacgacgatg attcagcttc tccaccgccg atctcgtctt cttacatgct      540
tctcgactc tctggaggaa gaggaggagc taacacggcg gttccaatgt ctaggaaacg      600
ttttaggacg aagtttagtc agtatcagaa ggagaagatg ttcgagttct cggagagagt      660
tggttgaggg atgccgaaag ctgatgacgt ggtgggtaag gagttttgtc gggagattgg      720
agttgataaa agcgttttca aagtgtggat gcataacaac aagatttcag gacgcagcgg      780
cgctagaaga gctaacggcg gagtagtagt aggaggagta ggagatagtc gtcagagtgt      840
tggtccgaca aatgggtcgt tttcttcgac gtgaggaaaa gaatggaaaag cgttgaaaaa      900
gcgtcgtcgt tttt                                           914
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<210> 48

<211> 271

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G2991 polypeptide Paralogous to G2999

<400> 48

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20

25

30

Ile Ser Phe Ser Asn Gly Lys Arg Cys His His His His Leu Ala Ser
 35 40 45

Glu Ala Val Ala Val Ala Thr Tyr Lys Glu Cys Leu Lys Asn His Ala
 50 55 60

Ala Gly Ile Gly Gly His Ala Leu Asp Gly Cys Gly Glu Phe Met Pro
 65 70 75 80

Ser Pro Ser Phe Asn Ser Asn Asp Pro Ala Ser Leu Thr Cys Ala Ala
 85 90 95

Cys Gly Cys His Arg Asn Phe His Arg Arg Glu Glu Asp Pro Ser Ser
 100 105 110

Leu Ser Ala Ile Val Pro Ala Ile Glu Phe Arg Pro His Asn Arg His
 115 120 125

Gln Leu Pro Pro Pro Pro Pro Pro His Leu Ala Gly Ile Arg Ser Pro
 130 135 140

Asp Asp Asp Asp Ser Ala Ser Pro Pro Pro Ile Ser Ser Ser Tyr Met
 145 150 155 160

Leu Leu Ala Leu Ser Gly Gly Arg Gly Gly Ala Asn Thr Ala Val Pro
 165 170 175

Met Ser Arg Lys Arg Phe Arg Thr Lys Phe Ser Gln Tyr Gln Lys Glu
 180 185 190

Lys Met Phe Glu Phe Ser Glu Arg Val Gly Trp Arg Met Pro Lys Ala
 195 200 205

Asp Asp Val Val Val Lys Glu Phe Cys Arg Glu Ile Gly Val Asp Lys
 210 215 220

Ser Val Phe Lys Val Trp Met His Asn Asn Lys Ile Ser Gly Arg Ser
 225 230 235 240

Gly Ala Arg Arg Ala Asn Gly Gly Val Val Val Gly Gly Val Gly Asp
 245 250 255

Ser Arg Gln Ser Val Val Pro Thr Asn Gly Ser Phe Ser Ser Thr
 260 265 270

<210> 49

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<211> 729
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G2992 Predicted polypeptide sequence is paralogous to G2999

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ctaactgtca ccggagaaat ggggtgttgt tacaaagagt gtttgaaaaa ccacgcggct      120
aatctcggcg gccatgctct cgacgggtgc ggcgagttta tgccgagtcc cacggctact      180
tccaccgatc cttcttctct ccgttgcgct gcttggtggt gccaccgtaa cttccaccgc      240
cgtgaccctt ccgagaatct caacttcctc accgcgcctc cgatttcttc tccctccggc      300
actgagtcgc cgccgtctcg tcacgtgtct tctcctgttc cttgctctta ctacacctca      360
gctcctccac atcacgtgat tctctctctc agctccgggt tccctggacc gtcagatcaa      420
gatccaacgg tggttaggtc agagaacagt tcaagaggag caatgaggaa acgaacaaga      480
accaaattca cgccggagca gaagatcaag atgagagcct tcgcagagaa agctgggttg      540
aaaatcaacg gatgtgatga aaagtcggtg agagagtttt gtaacgaagt tgggattgag      600
agaggagttc ttaaagtgtg gatgcataac aacaagtact cacttctcaa tggcaagatc      660
agagagatcg aacatggcct gtgtctgaac actcacagca atgatgggtga tgggtcttca      720
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<210> 50
<211> 242
<212> PRT
<213> Arabidopsis thaliana

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<220>
<223> G2992 polypeptide Paralogous to G2999

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<400> 50

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1          5          10          15

```

```

Ile Ala Gly Glu Leu Thr Val Thr Gly Glu Met Gly Val Cys Tyr Lys
          20          25          30

```

```

Glu Cys Leu Lys Asn His Ala Ala Asn Leu Gly Gly His Ala Leu Asp
          35          40          45

```

```

Gly Cys Gly Glu Phe Met Pro Ser Pro Thr Ala Thr Ser Thr Asp Pro
          50          55          60

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Ser Ser Leu Arg Cys Ala Ala Cys Gly Cys His Arg Asn Phe His Arg
          65          70          75          80

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Arg Asp Pro Ser Glu Asn Leu Asn Phe Leu Thr Ala Pro Pro Ile Ser
85 90 95

Ser Pro Ser Gly Thr Glu Ser Pro Pro Ser Arg His Val Ser Ser Pro
100 105 110

Val Pro Cys Ser Tyr Tyr Thr Ser Ala Pro Pro His His Val Ile Leu
115 120 125

Ser Leu Ser Ser Gly Phe Pro Gly Pro Ser Asp Gln Asp Pro Thr Val
130 135 140

Val Arg Ser Glu Asn Ser Ser Arg Gly Ala Met Arg Lys Arg Thr Arg
145 150 155 160

Thr Lys Phe Thr Pro Glu Gln Lys Ile Lys Met Arg Ala Phe Ala Glu
165 170 175

Lys Ala Gly Trp Lys Ile Asn Gly Cys Asp Glu Lys Ser Val Arg Glu
180 185 190

Phe Cys Asn Glu Val Gly Ile Glu Arg Gly Val Leu Lys Val Trp Met
195 200 205

His Asn Asn Lys Tyr Ser Leu Leu Asn Gly Lys Ile Arg Glu Ile Glu
210 215 220

His Gly Leu Cys Leu Asn Thr His Ser Asn Asp Gly Asp Gly Ser Ser
225 230 235 240

Ser Ser

<210> 51

<211> 1144

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G2993 Predicted polypeptide sequence is paralogous to G2999

<400> 51

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tattctcaag aaaggtttca ttttgagata aagtttgctg ctctttctgg ttgtggatag 180

atcaaaagaa tggagattgc aagtcaagaa gatcctattc caataaacac tagttatggt 240

aatagtggag gtgggcatgg gaacatgaac catcatcatc atgccaattc tgcaccatca 300

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 aaaaatcatg atcattctca tcatcatcat gtgggttaca acatcatggt taccaacatc 420
 aagaaagaga agcctgtggt gataaagtac aaggaatgcc taaagaacca tgcagctacc 480
 atgggaggca atgccattga tgggttgga gagtttatgc caagtgggtga agaagggtcc 540
 attgaagctc tcacttgctc agtttgcaac tgccatagaa actttcatag aagagaaacc 600
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 tata 1144

<210> 52
 <211> 310
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> G2993 polypeptide Paralogous to G2999

<400> 52

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 20 25 30

Asn Ser Ala Pro Ser Ser Leu Asn Ile Thr Thr Ser Asn Pro Leu Leu
 35 40 45

Val Ser Ser Asn Ser Asn Gly Leu Gly Lys Asn His Asp His Ser His
 50 55 60

His His His Val Gly Tyr Asn Ile Met Val Thr Asn Ile Lys Lys Glu
 65 70 75 80

Lys Pro Val Val Ile Lys Tyr Lys Glu Cys Leu Lys Asn His Ala Ala
 85 90 95

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Thr Met Gly Gly Asn Ala Ile Asp Gly Cys Gly Glu Phe Met Pro Ser
100 105 110

Gly Glu Glu Gly Ser Ile Glu Ala Leu Thr Cys Ser Val Cys Asn Cys
115 120 125

His Arg Asn Phe His Arg Arg Glu Thr Glu Gly Glu Glu Lys Thr Phe
130 135 140

Phe Ser Pro Tyr Leu Asn His His Gln Pro Pro Pro Gln Gln Arg Lys
145 150 155 160

Leu Met Phe His His Lys Met Ile Lys Ser Pro Leu Pro Gln Gln Met
165 170 175

Ile Met Pro Ile Gly Val Thr Thr Ala Gly Ser Asn Ser Glu Ser Glu
180 185 190

Asp Leu Met Glu Glu Glu Gly Gly Gly Ser Leu Thr Phe Arg Gln Pro
195 200 205

Pro Pro Pro Pro Ser Pro Tyr Ser Tyr Gly His Asn Gln Lys Lys Arg
210 215 220

Phe Arg Thr Lys Phe Thr Gln Glu Gln Lys Glu Lys Met Ile Ser Phe
225 230 235 240

Ala Glu Arg Val Gly Trp Lys Ile Gln Arg Gln Glu Glu Ser Val Val
245 250 255

Gln Gln Leu Cys Gln Glu Ile Gly Ile Arg Arg Arg Val Leu Lys Val
260 265 270

Trp Met His Asn Asn Lys Gln Asn Leu Ser Lys Lys Ser Asn Asn Val
275 280 285

Ser Asn Asn Val Asp Leu Ser Ala Gly Asn Asn Asp Ile Thr Glu Asn
290 295 300

Leu Ala Ser Thr Asn Pro
305 310

<210> 53
<211> 1083
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G2994 Predicted polypeptide sequence is paralogous to G2999
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atttggtggt ggtggtagtc atggtcacat gatccatcat catgatcatc atgctgctaa      180
ttctgctcct ccaactcaca acaacaacaa tactactcaa ccacctcaa tgccgttaca      240
tggtaatggt catggcaaca attatgatca tcatcatcat caagatcttc atcatgttgg      300
ttacaacgct atcatcaaga agcctatgat aaagtacaag gagtgtctca agaaccatgc      360
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gcccattgga gtctctaact accggtacat gcataacaac tccgagtccg aggactttat      660
ggaggaagat ggcgtaacca ccgcatctag atcgctacca aacctgccat acaaccagaa      720
gaagaggttc aggacaaagt tcacgccgga acagaaggag aagatgctta gttttgctga      780
gaaagttggg tggaaaatac aaaggcaaga agattgtgtt gttcaaaggt tttgtgaaga      840
gattggagtg aagagaagag tgcttaaggt ttggatgcac aacaacaaga tccatttctc      900
caagaagaac aacattaacc tcgaagacaa cgacaacgaa aagatcaaca atctcaacaa      960
tgttgatctg tccggttaata acgacatgac taagatcgtc ccatgatata attaataacg    1020
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aat                                                                    1083

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<210> 54
<211> 312
<212> PRT
<213> Arabidopsis thaliana

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<220>
<223> G2994 polypeptide Paralogous to G2999

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<400> 54

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Met Glu Ile Ala Ser Gln Glu Asp His Asp Met Pro Ile Pro Leu Asn
1           5           10           15

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Thr Thr Phe Gly Gly Gly Gly Ser His Gly His Met Ile His His His
20           25           30

```

```

Asp His His Ala Ala Asn Ser Ala Pro Pro Thr His Asn Asn Asn Asn
35           40           45

```

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Thr Thr Gln Pro Pro Pro Met Pro Leu His Gly Asn Gly His Gly Asn
Page 53

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305

310

<210> 55
<211> 782
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G2995 Predicted polypeptide sequence is paralogous to G2999

<400> 55
cagagtataa acgcactagt gagtgaaata agaatcagac atgagctcgt tatcaaaacc 60
aaacagacaa tttttgtcac caacaacaaa caaccaagac accggcagag aacaaacaat 120
cgcttgcgcc cgagatatgg ttgtcttgta caacgagtgc cttaaaaacc acgcggtcag 180
tctcggaggc cacgctcttg acggctgcgg tgagttcaca ccaaagtcaa ccaccatcct 240
cacggaccct ccgtccctta ggtgcatgac ttgtggctgc catcgcaact tccaccgtcg 300
tagtccttct gacggcttca gtcagcaccg gtcaccaccg tctccgttac agctgcagcc 360
actcgcccct gttccgaact tgcttctctc tcttagctcc ggtttctttg gaccctcgga 420
tcaagaagtc aagaacaaat ttacggtgga aagggatggt aggaagactg cgatgattaa 480
gaaacataag aggacgaaat tcacggcgga gcagaaggtg aagatgagag gtttcgcgga 540
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<210> 56
<211> 191
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G2995 polypeptide Paralogous to G2999

<400> 56

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1 5 10 15

Gly Gly His Ala Leu Asp Gly Cys Gly Glu Phe Thr Pro Lys Ser Thr
20 25 30

Thr Ile Leu Thr Asp Pro Pro Ser Leu Arg Cys Asp Ala Cys Gly Cys
35 40 45

His Arg Asn Phe His Arg Arg Ser Pro Ser Asp Gly Phe Ser Gln His
Page 55

50	55	60
Arg Ser Pro Pro Ser Pro Leu Gln Leu Gln Pro Leu Ala Pro Val Pro		
65	70	75 80
Asn Leu Leu Leu Ser Leu Ser Ser Gly Phe Phe Gly Pro Ser Asp Gln		
	85	90 95
Glu Val Lys Asn Lys Phe Thr Val Glu Arg Asp Val Arg Lys Thr Ala		
	100	105 110
Met Ile Lys Lys His Lys Arg Thr Lys Phe Thr Ala Glu Gln Lys Val		
	115	120 125
Lys Met Arg Gly Phe Ala Glu Arg Ala Gly Trp Lys Ile Asn Gly Trp		
	130	135 140
Asp Glu Lys Trp Val Arg Glu Phe Cys Ser Glu Val Gly Ile Glu Arg		
	145	150 155 160
Lys Val Leu Lys Val Trp Ile His Asn Asn Lys Tyr Phe Asn Asn Gly		
	165	170 175
Arg Ser Arg Asp Thr Thr Ser Ser Met Ser Leu Asn Leu Lys Leu		
	180	185 190

<210> 57
 <211> 886
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <223> G2996 Predicted polypeptide sequence is paralogous to G2999

<400> 57	
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gagcaagaag aggatatgaa tcttcatgag gaagaagaag acgacgacgc cgtttacgac	120
tctcctcctc tctctcgtgt tctcccaaaa gcctcgacag aaagtcatga aaccaccgga	180
actacttcca caggcggtgg cggaggattc atggttggtc acggcggtgg agggagcagg	240
tttaggttcc gtgagtgtct caagaaccaa gcggtgaaca taggaggaca cgcggtcgat	300
ggttggtggtg agtttatgcc agctggaatc gaaggtacca tcgacgctct aaaatgcgcc	360
gcttggtggct gtcaccgtaa cttccaccgc aaggaattac cttacttcca tcacgcgccg	420
ccacaacatc agcctcctcc tcccccgcca gggttttacc gtcttccagc tccggttagc	480
taccgaccac caccgtcaca agctcctcct cttcagctcg ctcttcccc tccacaaaga	540
gagagatcag aagatccaat ggagacgtct tcagctgaag caggaggagg gattaggaag	600

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 ggtgttccga gacaagttct taaggtttg ttacataaca acaaacacac tcttggttaag 780
 tcgccttcac cacttcatca tcatcaggct cctcctcctc caccaccaca gtcttcgttt 840
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<210> 58
 <211> 279
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> G2996 polypeptide Paralogous to G2999

<400> 58

Met Glu Phe Glu Asp Asn Asn Asn Asn Asn Asp Glu Glu Gln Glu Glu
 1 5 10 15

Asp Met Asn Leu His Glu Glu Glu Glu Asp Asp Asp Ala Val Tyr Asp
 20 25 30

Ser Pro Pro Leu Ser Arg Val Leu Pro Lys Ala Ser Thr Glu Ser His
 35 40 45

Glu Thr Thr Gly Thr Thr Ser Thr Gly Gly Gly Gly Gly Phe Met Val
 50 55 60

Val His Gly Gly Gly Gly Ser Arg Phe Arg Phe Arg Glu Cys Leu Lys
 65 70 75 80

Asn Gln Ala Val Asn Ile Gly Gly His Ala Val Asp Gly Cys Gly Glu
 85 90 95

Phe Met Pro Ala Gly Ile Glu Gly Thr Ile Asp Ala Leu Lys Cys Ala
 100 105 110

Ala Cys Gly Cys His Arg Asn Phe His Arg Lys Glu Leu Pro Tyr Phe
 115 120 125

His His Ala Pro Pro Gln His Gln Pro Pro Pro Pro Pro Gly Phe
 130 135 140

Tyr Arg Leu Pro Ala Pro Val Ser Tyr Arg Pro Pro Pro Ser Gln Ala
 145 150 155 160

Pro Pro Leu Gln Leu Ala Leu Pro Pro Pro Gln Arg Glu Arg Ser Glu
 165 170 175

Asp Pro Met Glu Thr Ser Ser Ala Glu Ala Gly Gly Gly Ile Arg Lys
180 185 190

Arg His Arg Thr Lys Phe Thr Ala Glu Gln Lys Glu Arg Met Leu Ala
195 200 205

Leu Ala Glu Arg Ile Gly Trp Arg Ile Gln Arg Gln Asp Asp Glu Val
210 215 220

Ile Gln Arg Phe Cys Gln Glu Thr Gly Val Pro Arg Gln Val Leu Lys
225 230 235 240

Val Trp Leu His Asn Asn Lys His Thr Leu Gly Lys Ser Pro Ser Pro
245 250 255

Leu His His His Gln Ala Pro Pro Pro Pro Pro Gln Ser Ser Phe
260 265 270

His His Glu Gln Asp Gln Pro
275

<210> 59
<211> 895
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G2997 Predicted polypeptide sequence is paralogous to G2999

<400> 59
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attgtagtac ggatgtctct tgagatgttc aagaattaag aaataaagaa agagggatcg 120
gagaatgaat tttgaggatc aagaagaaga tatggagatg tcagggtgta atccccctg 180
cggttacgac tctctaagcg gtgagggagc cacatctagt ggtggtggag gagtaggaag 240
gagtaaagga gttggagcga agataaggta tagagagtgc ttgaagaacc atgctgttaa 300
cataggtggc cagccgtgg acggttggtg cgagtttatg ccttccggtg aagatggaac 360
gctcgacgct cttaagtgtg cagcttgctg ctgccaccgc aacttccacc gcaaggaaac 420
cgaaagcatc ggcggtagag cccacagagt tcccacgtac tacaaccgcc cgccgcagcc 480
gcacagccg cctggatata ttcatttaac atctcccgcg gcgccttaca ggccaccgcg 540
ggcatcgggg gacgaggagg atacatcaaa tcctagcagc agcggcgagg ccacgaagag 600
gtttagaacg aagttcacgg cggaacagaa agagaagatg ttagcctttg cggagaggtt 660
ggggtggaga attcagaagc atgatgacgt ggcggttgag cagttctgtg cggagactgg 720
tgtaggaga caagtgtta aaatctggat gcataacaac aagaactctc ttggttaagaa 780

accctaattt tgctcgagac atgatttaaa acactagagg atcataattg tttctttttt 840
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<210> 60
 <211> 220
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> G2997 polypeptide Paralogous to G2999

<400> 60

Met Asn Phe Glu Asp Gln Glu Glu Asp Met Glu Met Ser Gly Val Asn
 1 5 10 15

Pro Pro Cys Gly Tyr Asp Ser Leu Ser Gly Glu Gly Ala Thr Ser Ser
 20 25 30

Gly Gly Gly Gly Val Gly Arg Ser Lys Gly Val Gly Ala Lys Ile Arg
 35 40 45

Tyr Arg Glu Cys Leu Lys Asn His Ala Val Asn Ile Gly Gly His Ala
 50 55 60

Val Asp Gly Cys Cys Glu Phe Met Pro Ser Gly Glu Asp Gly Thr Leu
 65 70 75 80

Asp Ala Leu Lys Cys Ala Ala Cys Gly Cys His Arg Asn Phe His Arg
 85 90 95

Lys Glu Thr Glu Ser Ile Gly Gly Arg Ala His Arg Val Pro Thr Tyr
 100 105 110

Tyr Asn Arg Pro Pro Gln Pro His Gln Pro Pro Gly Tyr Leu His Leu
 115 120 125

Thr Ser Pro Ala Ala Pro Tyr Arg Pro Pro Ala Ala Ser Gly Asp Glu
 130 135 140

Glu Asp Thr Ser Asn Pro Ser Ser Ser Gly Gly Thr Thr Lys Arg Phe
 145 150 155 160

Arg Thr Lys Phe Thr Ala Glu Gln Lys Glu Lys Met Leu Ala Phe Ala
 165 170 175

Glu Arg Leu Gly Trp Arg Ile Gln Lys His Asp Asp Val Ala Val Glu
 180 185 190

Gln Phe Cys Ala Glu Thr Gly Val Arg Arg Gln Val Leu Lys Ile Trp

Met His Asn Asn Lys Asn Ser Leu Gly Lys Lys Pro
210 215 220

<210> 61
<211> 930
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G2998 Predicted polypeptide sequence is paralogous to G2999

<400> 61
atggatatga gaagccatga aatgatagag agaagaagag aagacaatgg caacaacaat 60
ggtggtgttg ttattagtaa catcattagt actaatattg atgataattg caatggtaat 120
aacaacaaca ctctgtgtctc ttgcaactct caaaccttag atcaccacca atccaagtct 180
ccctcttcgt tttccatctc cgccgcagct aaaccacccg taagataccg tgagtgtcta 240
aagaatcatg cggcgagcgt cggcggaagt gttcacgacg gatgcggcga gtttatgccg 300
agtgggtgaag aaggaacaat cgaagctctc agatgcgctg cttgtgattg tcaccgtaat 360
ttccaccgga aagaaatgga cggcggttga agctcggatt tgatctctca ccaccgtcat 420
caccactacc accataacca atacggttga ggaggaggga gaagacctcc gccgccgaat 480
atgatgctta acccactcat gcttctctcc ccaccgaatt atcagccgat tcaccaccac 540
aagtatggaa tgagtcctcc cggaggagga ggaatggtga cgccgatgag cgttgcttac 600
ggcgggtggag gaggaggagc tgagtcgtct agtgaagatc tgaatctgta cggacaatca 660
agcggagaag gagctggtgc ggcggcgga caaatggcgt tttcgatgct gtcgtctaag 720
aaaagattca ggacaaagtt cacgacggat cagaaggaga ggatgatgga ctttgccgag 780
aagctagggg ggaggatgaa caagcaagac gaagaagagc ttaagagatt ctgcggcgag 840
atcggagtga agagacaagt cttcaaagtt tggatgcata acaacaagaa caatgctaag 900
aaaccaccaa caccaacaac tactctctaa 930

<210> 62
<211> 309
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G2998 polypeptide Paralogous to G2999

<400> 62

Met Asp Met Arg Ser His Glu Met Ile Glu Arg Arg Arg Glu Asp Asn
1 5 10 15

Gly Asn Asn Asn Gly Gly Val Val Ile Ser Asn Ile Ile Ser Thr Asn
Page 60

20

25

30

Ile Asp Asp Asn Cys Asn Gly Asn Asn Asn Asn Thr Arg Val Ser Cys
35 40 45

Asn Ser Gln Thr Leu Asp His His Gln Ser Lys Ser Pro Ser Ser Phe
50 55 60

Ser Ile Ser Ala Ala Ala Lys Pro Thr Val Arg Tyr Arg Glu Cys Leu
65 70 75 80

Lys Asn His Ala Ala Ser Val Gly Gly Ser Val His Asp Gly Cys Gly
85 90 95

Glu Phe Met Pro Ser Gly Glu Glu Gly Thr Ile Glu Ala Leu Arg Cys
100 105 110

Ala Ala Cys Asp Cys His Arg Asn Phe His Arg Lys Glu Met Asp Gly
115 120 125

Val Gly Ser Ser Asp Leu Ile Ser His His Arg His His His Tyr His
130 135 140

His Asn Gln Tyr Gly Gly Gly Gly Gly Arg Arg Pro Pro Pro Pro Asn
145 150 155 160

Met Met Leu Asn Pro Leu Met Leu Pro Pro Pro Pro Asn Tyr Gln Pro
165 170 175

Ile His His His Lys Tyr Gly Met Ser Pro Pro Gly Gly Gly Gly Met
180 185 190

Val Thr Pro Met Ser Val Ala Tyr Gly Gly Gly Gly Gly Gly Ala Glu
195 200 205

Ser Ser Ser Glu Asp Leu Asn Leu Tyr Gly Gln Ser Ser Gly Glu Gly
210 215 220

Ala Gly Ala Ala Ala Gly Gln Met Ala Phe Ser Met Ser Ser Ser Lys
225 230 235 240

Lys Arg Phe Arg Thr Lys Phe Thr Thr Asp Gln Lys Glu Arg Met Met
245 250 255

Asp Phe Ala Glu Lys Leu Gly Trp Arg Met Asn Lys Gln Asp Glu Glu
260 265 270

Glu Leu Lys Arg Phe Cys Gly Glu Ile Gly Val Lys Arg Gln Val Phe

Lys Val Trp Met His Asn Asn Lys Asn Asn Ala Lys Lys Pro Pro Thr
290 295 300

Pro Thr Thr Thr Leu
305

<210> 63
<211> 1064
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G3000 Predicted polypeptide sequence is paralogous to G2999

<400> 63
atgggtgata ggaaacaaac acacatacgt catcatcatc cttaatttct atttctcctt 60
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gacacaggaa cagtaaaca gatcatcagc tgatgataac tccggcggtt tacagcagta 540
acagctcgta caagccacgt gtaatgcac caacgggtga gattggacgg aggacttcat 600
cttcaagcga ggatatgaag aagattctga gtcacgtaa ccaaacggt gatgggaaaa 660
gtttgatgat gatgatgat aggaagaaga agagagtgag gacaaagatc aatgaagaac 720
aaaaggagaa gatgaaggaa tttgcagaga gattaggggtg gaggatgcag aagaaagatg 780
aagaagagat tgataagttt tgtaggatgg tgaatctgag gagacaagtt tttaaggttt 840
ggatgcataa taacaagcaa gcaatgaaga gaaacaatag taacattagt gaatagtttg 900
atgatctgat aaaagtga aaatatttta caatcctggt ttgcttttat atataatttt 960
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gttttatatt gtatctggga ttattttttt cttttactaa aaaa 1064

<210> 64
<211> 249
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G3000 polypeptide Paralogous to G2999

<400> 64

Met Glu Leu Gly Gly Lys Cys Asn Ala Ile Thr Thr Thr Thr Met Ile
 1 5 10 15

Ser Thr Glu Val Lys Pro His Thr Asp Pro Glu Pro Glu Ala Lys Pro
 20 25 30

Glu Ser Asp Pro Ser Met Ala Leu Phe Pro Ile Lys Lys Glu Asn Gln
 35 40 45

Lys Pro Lys Thr Arg Val Asp Gln Gly Ala Lys Tyr Arg Glu Cys Gln
 50 55 60

Lys Asn His Ala Ala Ser Thr Gly Gly His Val Val Asp Gly Cys Cys
 65 70 75 80

Glu Phe Met Ala Gly Gly Glu Glu Gly Thr Leu Gly Ala Leu Lys Cys
 85 90 95

Ala Ala Cys Asn Cys His Arg Ser Phe His Arg Lys Glu Val Tyr Gly
 100 105 110

His Arg Asn Ser Lys Gln Asp His Gln Leu Met Ile Thr Pro Ala Phe
 115 120 125

Tyr Ser Ser Asn Ser Ser Tyr Lys Pro Arg Val Met His Pro Thr Gly
 130 135 140

Glu Ile Gly Arg Arg Thr Ser Ser Ser Ser Glu Asp Met Lys Lys Ile
 145 150 155 160

Leu Ser His Arg Asn Gln Asn Val Asp Gly Lys Ser Leu Met Met Met
 165 170 175

Met Met Arg Lys Lys Lys Arg Val Arg Thr Lys Ile Asn Glu Glu Gln
 180 185 190

Lys Glu Lys Met Lys Glu Phe Ala Glu Arg Leu Gly Trp Arg Met Gln
 195 200 205

Lys Lys Asp Glu Glu Glu Ile Asp Lys Phe Cys Arg Met Val Asn Leu
 210 215 220

Arg Arg Gln Val Phe Lys Val Trp Met His Asn Asn Lys Gln Ala Met
 225 230 235 240

Lys Arg Asn Asn Ser Asn Ile Ser Glu

245

<210> 65
<211> 862
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G3001 Predicted polypeptide sequence is paralogous to G2999

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atgtataaat aacaagctca tt 862

<210> 66
<211> 242
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G3001 polypeptide Paralogous to G2999

<400> 66
Met Asp Glu Ile Lys Pro Lys Lys Glu Glu Asn Ser Lys Arg Arg Arg
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20 25 30
Pro Thr Cys Lys Thr Lys Pro Lys Pro Thr Arg Thr His His Ala Pro
35 40 45

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Pro Pro Ile Leu Asp Ser Ile Phe Lys Val Thr His Lys Pro His Tyr
50 55 60

Tyr Glu Cys Arg Lys Asn His Ala Ala Asp Ile Gly Thr Thr Ala Tyr
65 70 75 80

Asp Gly Cys Gly Glu Phe Val Ser Ser Thr Gly Glu Glu Asp Ser Leu
85 90 95

Asn Cys Ala Ala Cys Gly Cys His Arg Asn Phe His Arg Glu Glu Leu
100 105 110

Ile Pro Glu Asn Gly Gly Val Thr Glu Thr Val Leu Glu Val Leu Lys
115 120 125

Ile Ser Ser Cys Gln Phe Arg Arg Ile Phe Cys Ser Pro Tyr Gly Gly
130 135 140

Gly Lys Ser Glu Gly Lys Lys Lys Lys Lys Glu Lys Glu Ser Tyr Gly
145 150 155 160

Gly Asp Pro Ile Ile Lys Asp Arg Phe Gly Gly Ala Glu Glu Glu Glu
165 170 175

Gly Ile Val Lys Arg Leu Lys Thr Lys Phe Thr Ala Glu Gln Thr Glu
180 185 190

Lys Met Arg Asp Tyr Ala Glu Lys Leu Arg Trp Lys Val Arg Pro Glu
195 200 205

Arg Gln Glu Glu Val Glu Glu Phe Cys Val Glu Ile Gly Val Asn Arg
210 215 220

Lys Asn Phe Arg Ile Trp Met Asn Asn His Lys Asp Lys Ile Ile Ile
225 230 235 240

Asp Glu

<210> 67

<211> 721

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G3002 Predicted polypeptide sequence is paralogous to G2999

<400> 67

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a 721

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<210> 68
<211> 168
<212> PRT
<213> Arabidopsis thaliana

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<220>
<223> G3002 polypeptide Paralogous to G2999
<400> 68

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Met Gln Ser Thr Cys Val Tyr Arg Glu Cys Met Arg Asn His Ala Ala
1           5           10           15

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Lys Leu Gly Ser Tyr Ala Ile Asp Gly Cys Arg Glu Tyr Ser Gln Pro
          20           25           30

```

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Ser Thr Gly Asp Leu Cys Val Ala Cys Gly Cys His Arg Ser Tyr His
          35           40           45

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```

Arg Arg Ile Asp Val Ile Ser Ser Pro Gln Ile Asn His Thr Arg Phe
          50           55           60

```

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Pro Phe Thr Ser Leu Arg Arg Val Lys Gln Leu Ala Arg Leu Lys Trp
65           70           75           80

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```

Lys Thr Ala Glu Glu Arg Asn Glu Glu Glu Glu Asp Asp Thr Glu Glu
          85           90           95

```

```

Thr Ser Thr Glu Glu Lys Met Thr Val Gln Arg Arg Arg Lys Ser Lys
          100          105          110

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Phe Thr Ala Glu Gln Arg Glu Ala Met Lys Asp Tyr Ala Ala Lys Leu
          115          120          125

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115

120

125

Gly Trp Thr Leu Lys Asp Lys Arg Ala Leu Arg Glu Glu Ile Arg Val
130 135 140

Phe Cys Glu Gly Ile Gly Val Thr Arg Tyr His Phe Lys Thr Trp Val
145 150 155 160

Asn Asn Asn Lys Lys Phe Tyr His
165

<210> 69
<211> 579
<212> DNA
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3380 Predicted polypeptide sequence is orthologous to G1792 Orthologous to G1792

<400> 69
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gtgggtcgcaa tcgatcgatc gatatcatgg acggcgacgg cggcggcgga tgggacgatc 120
agggcaacgg cggcggcgag acgaccaagt accgtggcgt gcgtcgccgg ccttctggca 180
agttcgcggc ggagatccgt gactccagca ggcagagcgt ccgcgtctgg ctgggaacct 240
tcgacaccgc cgaggaggct gcgcgggctt acgaccgcgc cgctacgcc atgcgcggcc 300
acctcgccgt cctcaacttc cctgctgagg cgcgcaacta cgtgcgggga tcaggctcgt 360
cgctctcgtc ccgacagcat cagcagcggc aggtgatcga gctggagtgc ctagacgacc 420
aagtgctgca agagatgctc aagggtggcg acgatcagta caggtcagca gctgggagca 480
agaggaataa ctactagcta tatatgctgc taacctactt acaatcgcca tacatatcga 540
ggtttgggga ttttcttctc acctgtgtgc agaggctgc 579

<210> 70
<211> 136
<212> PRT
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3380 polypeptide Orthologous to G1792

<400> 70

Met Asp Gly Asp Gly Gly Gly Gly Trp Asp Asp Gln Gly Asn Gly Gly
1 5 10 15

Gly Glu Thr Thr Lys Tyr Arg Gly Val Arg Arg Arg Pro Ser Gly Lys
20 25 30

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Phe Ala Ala Glu Ile Arg Asp Ser Ser Arg Gln Ser Val Arg Val Trp
35 40 45

Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Arg
50 55 60

Ala Ala Tyr Ala Met Arg Gly His Leu Ala Val Leu Asn Phe Pro Ala
65 70 75 80

Glu Ala Arg Asn Tyr Val Arg Gly Ser Gly Ser Ser Ser Ser Ser Arg
85 90 95

Gln His Gln Gln Arg Gln Val Ile Glu Leu Glu Cys Leu Asp Asp Gln
100 105 110

Val Leu Gln Glu Met Leu Lys Gly Gly Asp Asp Gln Tyr Arg Ser Ala
115 120 125

Ala Gly Ser Lys Arg Asn Asn Tyr
130 135

<210> 71
<211> 514
<212> DNA
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3381 Predicted polypeptide sequence is orthologous to G1792

<400> 71
atcgatcatc tgctacgaac tcaccctata tatatataact ccatcttagg agctgcttga 60
tcgatcgaca tatatataac taatggatca tcatcatcag cagcagcagc aggaggggtga 120
gctggtggcc aagtacaggg gcgtgcggcg gcggccgtgg ggcaaattcg cggcagagat 180
ccgcgactcg agccggcacg gcgtccgcgt gtggctgggc accttcgaca cagccgagga 240
ggccgctcgc gcctacgacc gctccgccta ctccatgcgc ggcgccaacg ccgtcctcaa 300
cttccccgcc gacgcccaca tctacgcccg tcaactacac aataataacg ccgctgctgg 360
ctcttcatct tcctcttccg ccgcccgcgc agcagccagg ccgcccgcga tcgagttcga 420
gtacctcgat gaccacgtcc tgcaggagat gctccgagac cacaccacca acaagtagct 480
tactactcca ctatatatgc tgctgctgc ttgt 514

<210> 72
<211> 131
<212> PRT
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3381 polypeptide Orthologous to G1792

<400> 72

Met Asp His His His Gln Gln Gln Gln Gln Glu Gly Glu Leu Val Ala
1 5 10 15

Lys Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu
20 25 30

Ile Arg Asp Ser Ser Arg His Gly Val Arg Val Trp Leu Gly Thr Phe
35 40 45

Asp Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Arg Ser Ala Tyr Ser
50 55 60

Met Arg Gly Ala Asn Ala Val Leu Asn Phe Pro Ala Asp Ala His Ile
65 70 75 80

Tyr Ala Arg Gln Leu His Asn Asn Asn Ala Ala Ala Gly Ser Ser Ser
85 90 95

Ser Ser Ser Ala Ala Ala Ala Ala Ala Arg Pro Pro Pro Ile Glu Phe
100 105 110

Glu Tyr Leu Asp Asp His Val Leu Gln Glu Met Leu Arg Asp His Thr
115 120 125

Thr Asn Lys
130

<210> 73

<211> 375

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3383 Predicted polypeptide sequence is orthologous to G1792

<400> 73

atggaggaca accggagcaa ggacacggcg accaagtacc gcggcgtgag gaggcggccg	60
tggggcaagt tcgcggcgga gatccgcgac ccggagcgcg gcggggcgcg cgtctggctc	120
ggcaccttcg acaccgccga ggaggcggcg cgtgcctacg accgcgcggc ctacgccag	180
cgcggcgccc cgcgcgtgct caacttcccg gccgcgcgcg ccgccggcag gggcggagga	240
gccggcggcg ccgcttcggg gtcgtcgtcg tcgtcgtccg cgcagcgcgg caggggcgac	300
aagatcgagt tcgagtacct cgacgacaag gtgctcgacg atctcctcga cgacgagaag	360
taccgtggta aatga	375

<210> 74

<211> 124

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3383 polypeptide Orthologous to G1792

<400> 74

Met Glu Asp Asn Arg Ser Lys Asp Thr Ala Thr Lys Tyr Arg Gly Val
1 5 10 15

Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile Arg Asp Pro Glu
20 25 30

Arg Gly Gly Ala Arg Val Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu
35 40 45

Ala Ala Arg Ala Tyr Asp Arg Ala Ala Tyr Ala Gln Arg Gly Ala Ala
50 55 60

Ala Val Leu Asn Phe Pro Ala Ala Ala Ala Ala Gly Arg Gly Gly Gly
65 70 75 80

Ala Gly Gly Ala Ala Ser Gly Ser Ser Ser Ser Ser Ser Ala Gln Arg
85 90 95

Gly Arg Gly Asp Lys Ile Glu Phe Glu Tyr Leu Asp Asp Lys Val Leu
100 105 110

Asp Asp Leu Leu Asp Asp Glu Lys Tyr Arg Gly Lys
115 120

<210> 75

<211> 466

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3515 Predicted polypeptide sequence is orthologous to G1792

<400> 75

gtgtgcgagc ggttgcgctcc gcatggagga cgacaagagt aaggagggga aatcgctcgtc 60

gtcgtaccgc ggcgtgcgga agcggccgtg gggcaagtgc gcggcgagga tccgcgaccc 120

ggagcgcggg ggagcccgcg tgtggctcgg caggttcgac acccgaggagg aggccgcgcg 180

ggcgtacgac cgcgccgcat tcgcatgaa gggcgccacg gccatgctca acttcccggg 240

agatcatcat cacggcgccg caagcaggat gaccagcacc ggctcttctt cgtcctcctt 300

caccacgcct cctccggcga actcctccgc ggcggcgggc cgcggcggt cccgatcggac 360

gacggacaag gtggagctgg agtgccctga cgacaaggct ctggaggacc tcctcgcgga 420

gaccaactat cgtgataaga actactagct agctagctac tatggc 466

<210> 76
 <211> 141
 <212> PRT
 <213> Oryza sativa (japonica cultivar-group)

<220>
 <223> G3515 polypeptide Orthologous to G1792

<400> 76

Met Glu Asp Asp Lys Ser Lys Glu Gly Lys Ser Ser Ser Ser Tyr Arg
 1 5 10 15

Gly Val Arg Lys Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile Arg Asp
 20 25 30

Pro Glu Arg Gly Gly Ala Arg Val Trp Leu Gly Thr Phe Asp Thr Ala
 35 40 45

Glu Glu Ala Ala Arg Ala Tyr Asp Arg Ala Ala Phe Ala Met Lys Gly
 50 55 60

Ala Thr Ala Met Leu Asn Phe Pro Gly Asp His His His Gly Ala Ala
 65 70 75 80

Ser Arg Met Thr Ser Thr Gly Ser Ser Ser Ser Ser Phe Thr Thr Pro
 85 90 95

Pro Pro Ala Asn Ser Ser Ala Ala Ala Gly Arg Gly Gly Ser Asp Arg
 100 105 110

Thr Thr Asp Lys Val Glu Leu Glu Cys Leu Asp Asp Lys Val Leu Glu
 115 120 125

Asp Leu Leu Ala Glu Thr Asn Tyr Arg Asp Lys Asn Tyr
 130 135 140

<210> 77
 <211> 393
 <212> DNA
 <213> Zea mays

<220>
 <223> G3516 Predicted polypeptide sequence is orthologous to G1792

<400> 77

atggaggacg acaagaagga gggcaagtac cgcggcgtgc ggaagcggcc gtggggcaag 60
 ttgccgcgag agatccggga cccggagcgc ggcggctccc gcgtctggct cggcaccttc 120
 gacaccgccc aggaggccgc cagggcctac gaccgcgccc cattcgccat gaagggcgcc 180
 acggccgtgc tcaacttccc cgccagcggg ggatcgctcag ctggcgcggc tcccggcggc 240

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cggaccagcg gcggctcctc ctgctccacc acgtcggttc cggccagcag ggggagggcc 300
 cgtgttccccg actcggagaa ggtggagctg gagtgcctcg acgacagggt cttggaagag 360
 ctgctcgcgg aagacaagta caacaagaac taa 393

<210> 78
 <211> 130
 <212> PRT
 <213> Zea mays

<220>
 <223> G3516 polypeptide Orthologous to G1792

<400> 78

Met Glu Asp Asp Lys Lys Glu Gly Lys Tyr Arg Gly Val Arg Lys Arg
 1 5 10 15

Pro Trp Gly Lys Phe Ala Ala Glu Ile Arg Asp Pro Glu Arg Gly Gly
 20 25 30

Ser Arg Val Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Arg
 35 40 45

Ala Tyr Asp Arg Ala Ala Phe Ala Met Lys Gly Ala Thr Ala Val Leu
 50 55 60

Asn Phe Pro Ala Ser Gly Gly Ser Ser Ala Gly Ala Ala Pro Gly Gly
 65 70 75 80

Arg Thr Ser Gly Gly Ser Ser Ser Ser Thr Thr Ser Ala Pro Ala Ser
 85 90 95

Arg Gly Arg Ala Arg Val Pro Asp Ser Glu Lys Val Glu Leu Glu Cys
 100 105 110

Leu Asp Asp Arg Val Leu Glu Glu Leu Leu Ala Glu Asp Lys Tyr Asn
 115 120 125

Lys Asn
 130

<210> 79
 <211> 477
 <212> DNA
 <213> Zea mays

<220>
 <223> G3517 Predicted polypeptide sequence is orthologous to G1792

<400> 79

tacgtccgat ccacagccat catcgccacc cgcgcgctta tggatggcga gtggtccaag 60

gacggcggag gcggcgagcc gaccaagtac cgcggcgtgc ggcgtcggcc ctggggcaag 120
 tacgcggcgg agatccgcga ctcgagccgg cacggcgctcc gcatctggct cggcacgttc 180
 gacaccgccg aggaggccgc cagggcgtag gaccgctccg ccaactccat gcgcggcgcc 240
 aacgccgtgc tcaacttccc ggaggacgcg cccgcctacg ccgcgcggcc ctcccggtggc 300
 tccgcggcgg gatcctcgtc cagaccggcg ggctccggcc gggacgtgat cgagtttgag 360
 tacctcgacg acgaggtgct gcaggagatg ctgaggagcc aggagccgct gcgcggcgccg 420
 gcgcagaaga agaagtagcg cgagcgccac aggtggcgaa acggccgctt ttccaaa 477

<210> 80
 <211> 132
 <212> PRT
 <213> Zea mays

<220>
 <223> G3517 polypeptide Orthologous to G1792

<400> 80

Met Asp Gly Glu Trp Ser Lys Asp Gly Gly Gly Gly Glu Pro Thr Lys
 1 5 10 15

Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Tyr Ala Ala Glu Ile
 20 25 30

Arg Asp Ser Ser Arg His Gly Val Arg Ile Trp Leu Gly Thr Phe Asp
 35 40 45

Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Arg Ser Ala Asn Ser Met
 50 55 60

Arg Gly Ala Asn Ala Val Leu Asn Phe Pro Glu Asp Ala Pro Ala Tyr
 65 70 75 80

Ala Ala Ala Ala Ser Arg Gly Ser Ala Gly Gly Ser Ser Ser Arg Pro
 85 90 95

Ala Gly Ser Gly Arg Asp Val Ile Glu Phe Glu Tyr Leu Asp Asp Glu
 100 105 110

Val Leu Gln Glu Met Leu Arg Ser Gln Glu Pro Ser Ala Ala Ala Ala
 115 120 125

Gln Lys Lys Lys
 130

<210> 81
 <211> 717

<212> DNA

<213> Glycine max

<220>

<223> G3518 Predicted polypeptide sequence is orthologous to G1792

<400> 81

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ctaacacaca taacaataac ttagcaacat tttttccttc cttctttctt tctttctata      60
ctttttgttg ttaattctaa gttctaagag aagaaaaatg gaggggtggaa gatcatcagt    120
ttcaaatggg aatgttgagg ttcgttatag agggattaga agaaggccat ggggaaagtt    180
tgcagcagag attcgtgacc ctacaaggaa aggaacaagg atatggcttg gaacatttga    240
cactgctgaa caagctgcac gagcttatga tgctgctgct tttcattttc gtggccacag    300
agcaattctc aacttcccaa atgagtatca atctcataat ccaaactctt ctttgcctat    360
gcctctagct gtgtcagctc ctctttctta ttctttcttct tcttccactt ctaattattc    420
cggtgatgat aataataacc accttgtagag accagctttt tctggagaaa taatgcaagg    480
tggtgatcat gatgatgata cttttgagtt ggagtacttc gataataagt tgctcgagga    540
actccttcag atgcaagata acagacactt ctaaaagtaa aatataacac aagccagcta    600
tgttgtgtta gtcactggca tgaaataaaa tgcaaagaaa tattgttgat tttatttaat    660
atattttggt tgattttttt tttttttttt gtagctgata aaagttcttc gaaatga      717

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<210> 82

<211> 158

<212> PRT

<213> Glycine max

<220>

<223> G3518 polypeptide Orthologous to G1792

<400> 82

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Met Glu Gly Gly Arg Ser Ser Val Ser Asn Gly Asn Val Glu Val Arg
1              5              10              15

```

```

Tyr Arg Gly Ile Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile
          20              25              30

```

```

Arg Asp Pro Thr Arg Lys Gly Thr Arg Ile Trp Leu Gly Thr Phe Asp
          35              40              45

```

```

Thr Ala Glu Gln Ala Ala Arg Ala Tyr Asp Ala Ala Ala Phe His Phe
          50              55              60

```

```

Arg Gly His Arg Ala Ile Leu Asn Phe Pro Asn Glu Tyr Gln Ser His
65              70              75              80

```

```

Asn Pro Asn Ser Ser Leu Pro Met Pro Leu Ala Val Ser Ala Pro Pro
          85              90              95

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Ser Tyr Ser Ser Ser Ser Ser Thr Ser Asn Tyr Ser Gly Asp Asp Asn
100 105 110

Asn Asn His Leu Val Arg Pro Ala Phe Ser Gly Glu Ile Met Gln Gly
115 120 125

Gly Asp His Asp Asp Asp Thr Phe Glu Leu Glu Tyr Phe Asp Asn Lys
130 135 140

Leu Leu Glu Glu Leu Leu Gln Met Gln Asp Asn Arg His Phe
145 150 155

<210> 83

<211> 609

<212> DNA

<213> Glycine max

<220>

<223> G3519 Predicted polypeptide sequence is orthologous to G1792

<400> 83

tttcttttctt tctatacttt ttgtggttct gattattaag ttctaagaga ataacaatgg	60
agggtggaag atcatctggt tcaaattgga attgtgaggt tcggtataga gggattagaa	120
gaaggccatg gggcaagttt gcagcagaga ttcgtgacct tacgaggaaa gggacaagga	180
tatggcttgg aacatttgac actgcggaac aagctgctcg agcttatgat gctgctgctt	240
ttcatttttcg tgggtcataga gcaattctca acttcccaaa tgagtaccaa tctcataatc	300
caaactcttc tttgcctatg cctctaattg tgctctctcc ttcttattct tcttctttca	360
cttctaatta ttctgctgat gataataacc acctgtgtgag acctggagaa ataatgcaag	420
gtggtgatct tgatgacact tttaggttgg agtacttggg taataagttg ctcgaggaac	480
tccttcagat gcaagataac agacacttct aaaagtaaaa tataacacaa gccagctatg	540
ttgtgttagt cactggcatg aaataaaatg caaagaaata ttgttgattt tatttaatat	600
attttgttt	609

<210> 84

<211> 151

<212> PRT

<213> Glycine max

<220>

<223> G3519 polypeptide Orthologous to G1792

<400> 84

Met Glu Gly Gly Arg Ser Ser Val Ser Asn Gly Asn Cys Glu Val Arg
1 5 10 15

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Tyr Arg Gly Ile Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile
20 25 30

Arg Asp Pro Thr Arg Lys Gly Thr Arg Ile Trp Leu Gly Thr Phe Asp
35 40 45

Thr Ala Glu Gln Ala Ala Arg Ala Tyr Asp Ala Ala Ala Phe His Phe
50 55 60

Arg Gly His Arg Ala Ile Leu Asn Phe Pro Asn Glu Tyr Gln Ser His
65 70 75 80

Asn Pro Asn Ser Ser Leu Pro Met Pro Leu Ile Val Pro Pro Pro Ser
85 90 95

Tyr Ser Ser Ser Phe Thr Ser Asn Tyr Ser Ala Asp Asp Asn Asn His
100 105 110

Leu Val Arg Pro Gly Glu Ile Met Gln Gly Gly Asp Leu Asp Asp Thr
115 120 125

Phe Glu Leu Glu Tyr Leu Asp Asn Lys Leu Leu Glu Glu Leu Leu Gln
130 135 140

Met Gln Asp Asn Arg His Phe
145 150

<210> 85
<211> 440
<212> DNA
<213> Glycine max

<220>
<223> G3520 Predicted polypeptide sequence is orthologous to G1792

<400> 85
aaggcacaca atggaagagg agtcaaagga gaaaaagaag gacactaagg aggaaccacg 60
ttatagagga gtgcggcggc ggccgtgggg gaagttcgcg gccgagattc gggaccggc 120
ccggcacggt gcccgagtgt ggctggggac atttctcacg gcggaggagg ctgctagggc 180
ttatgaccga gctgcctatg agatgagggg cgcttttagcc gttctcaatt ttccaaatga 240
gtatccttca tgctcttcta tgaactcatc ttcaacatta gcaccttcat cttcttcttc 300
aaattcaatg cttaaaagtg atcatggtaa acaagttatt gagttcgagt gcttggatga 360
caaattgtta gaggaccttc ttgattgtga tgactatgcc tacgagaaag acttgcctaa 420
gaactgaacg gtttgatcaa 440

<210> 86
<211> 138

<212> PRT

<213> Glycine max

<220>

<223> G3520 polypeptide Orthologous to G1792

<400> 86

Met Glu Glu Glu Ser Lys Glu Lys Lys Lys Asp Thr Lys Glu Glu Pro
1 5 10 15

Arg Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu
20 25 30

Ile Arg Asp Pro Ala Arg His Gly Ala Arg Val Trp Leu Gly Thr Phe
35 40 45

Leu Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Arg Ala Ala Tyr Glu
50 55 60

Met Arg Gly Ala Leu Ala Val Leu Asn Phe Pro Asn Glu Tyr Pro Ser
65 70 75 80

Cys Ser Ser Met Asn Ser Ser Ser Thr Leu Ala Pro Ser Ser Ser Ser
85 90 95

Ser Asn Ser Met Leu Lys Ser Asp His Gly Lys Gln Val Ile Glu Phe
100 105 110

Glu Cys Leu Asp Asp Lys Leu Leu Glu Asp Leu Leu Asp Cys Asp Asp
115 120 125

Tyr Ala Tyr Glu Lys Asp Leu Pro Lys Asn
130 135

<210> 87

<211> 1082

<212> DNA

<213> Glycine max

<220>

<223> G3643 Predicted polypeptide sequence is orthologous to G47

<400> 87

ccacgcgtcc gcttcttctc tcagaataca caacacaaag tcaatataat tatagtatat 60

ccctatgagt aggagttcgg c gatgcatgg aattacaagc acaaacaaca agttgaaggg 120

agttcggcgt cgaaaatggg gcaaattgggt gtcggagatt cgtgttccgg gcacgcaaga 180

gcgtttgtgg ttgggaacct acgccacgcc ggaggctgcc gcggtggctc acgacgttgc 240

cgtctactgt ctaagtaggc cttcttcggt ggacaaactt aacttccccg aaaccttgtc 300

ttcgtacagt gttcagctca gggacatgtc tccgaggtct gtgcagaagg tggcttccga 360

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 agaaactaat tgcgagagtg atgagaggac tagtactgcg tctgtgtgta atgttggttg 480
 agaagggtggt gctgatcatt cggatgtgtt ttggtgggat gatgatggtg ggtcttggca 540
 tggaagtggg ggagattcta cggaaaggga tgccttgagc atttccattg aagattatct 600
 ttagctgttc taggtttcaa ctttagttat cttttttttt ttttttttga gttatgatcg 660
 atgcgcatag ttagtagtta cagataatta ctgctagtgt tgggtgttta aacggtcaga 720
 gatgatgata tataaatttg atgtgcgcta gctgcctttt tgaagaaact aaaaaaaggt 780
 aaaacaagaa agattgtacc cccaaaatga acttgggtcaa tttcacactt tcacgccatt 840
 tgcattttgt gcacgttggt agttttcaaa ttgttaattc ccttgctaaa cccactcaaa 900
 cttgagtgcg ttcacctttt attaccacgt agtaactgag agttaacgaa aatatttctt 960
 tataaaaatt atttaccatt tagtgtcttt cgtttacttg taattattca acttgtcaat 1020
 aagatgaaag ttctaatttt agatataata aaattcagct agtatttgtg aattactcac 1080
 tt 1082

<210> 88
 <211> 179
 <212> PRT
 <213> Glycine max

<220>
 <223> G3643 polypeptide Orthologous to G47
 <400> 88

Met	Ser	Arg	Ser	Ser	Ala	Met	His	Gly	Ile	Thr	Ser	Thr	Asn	Asn	Lys
1				5					10					15	
Leu	Lys	Gly	Val	Arg	Arg	Arg	Lys	Trp	Gly	Lys	Trp	Val	Ser	Glu	Ile
			20					25					30		
Arg	Val	Pro	Gly	Thr	Gln	Glu	Arg	Leu	Trp	Leu	Gly	Thr	Tyr	Ala	Thr
		35					40					45			
Pro	Glu	Ala	Ala	Ala	Val	Ala	His	Asp	Val	Ala	Val	Tyr	Cys	Leu	Ser
	50					55					60				
Arg	Pro	Ser	Ser	Leu	Asp	Lys	Leu	Asn	Phe	Pro	Glu	Thr	Leu	Ser	Ser
65					70					75				80	
Tyr	Ser	Val	Gln	Leu	Arg	Asp	Met	Ser	Pro	Arg	Ser	Val	Gln	Lys	Val
				85					90					95	
Ala	Ser	Asp	Val	Gly	Met	Asp	Val	Asp	Ala	Arg	Asn	Ile	Val	Ala	Gly
			100					105					110		

Lys Thr Ser Thr Val Gly Ala Glu Thr Asn Cys Glu Ser Asp Glu Arg
115 120 125

Thr Ser Thr Ala Ser Val Cys Asn Val Val Gly Glu Gly Gly Ala Asp
130 135 140

His Ser Asp Val Phe Trp Trp Asp Asp Asp Gly Gly Ser Trp His Gly
145 150 155 160

Ser Gly Gly Asp Ser Thr Glu Arg Asp Ala Leu Ser Ile Ser Ile Glu
165 170 175

Asp Tyr Leu

<210> 89
<211> 687
<212> DNA
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3644 Predicted polypeptide sequence is orthologous to G47

<400> 89
atgccttttg tacgtacact tgctttccca acgctcgcga atcaaatacga ggggtgaaatt 60
aagtcaagaa cggagagaga tcacgggtgag gttgatctca gctcgccgga ggaggcaatg 120
agccgggcgag agtgcgggcg cggcgaggag gaggagcggg gcagggtacag gggcggtgcg 180
cggcgggcggt ggggggaagt ggtgtcggag atccgggtgc ccggcacgcg ggagcggctg 240
tggtctggggg cctacgccac gccggaggcc gccgccgtcg cgcacgacac ggccgtctac 300
ttcctccgcg gaggcgcggg cgacggcggt ggcgggcgcg cgacgctcaa cttcccggag 360
cgcgcgggcg ccacgtacgg cggcgggcgcc gccgtggcgc gcctgtcgcc gcgggtccgtg 420
cagcgcggtg cgtccgacgc cggcatggcc gccgacgcgc agctcgtggc ggcgcgggac 480
gccgcgcccc cgcccgcgcc ggcgacggcg tacgcgcgcc cggatcactg cgccggcgcg 540
acgacggcgc ggcacgacga gctggcgcg cgcgggatgt acggcgctca cgcgcatgcc 600
gccggcgcg acgccaggac gagcgggcg cggcagctcg tctgtgccga ggagattagc 660
gtggatgaca tggagatcct gatgtaa 687

<210> 90
<211> 228
<212> PRT
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3644 polypeptide Orthologous to G47

<400> 90

Met Pro Phe Val Arg Thr Leu Ala Phe Pro Thr Leu Ala Asn Gln Ile
 1 5 10 15

Glu Gly Glu Ile Lys Ser Arg Thr Glu Arg Asp His Gly Glu Val Asp
 20 25 30

Leu Ser Ser Pro Glu Glu Ala Met Ser Arg Ala Glu Cys Gly Gly Gly
 35 40 45

Glu Glu Glu Glu Arg Cys Arg Tyr Arg Gly Val Arg Arg Arg Arg Trp
 50 55 60

Gly Lys Trp Val Ser Glu Ile Arg Val Pro Gly Thr Arg Glu Arg Leu
 65 70 75 80

Trp Leu Gly Ser Tyr Ala Thr Pro Glu Ala Ala Ala Val Ala His Asp
 85 90 95

Thr Ala Val Tyr Phe Leu Arg Gly Gly Ala Gly Asp Gly Gly Gly Gly
 100 105 110

Gly Ala Thr Leu Asn Phe Pro Glu Arg Ala Ala Ala Thr Tyr Gly Gly
 115 120 125

Gly Ala Ala Val Ala Arg Leu Ser Pro Arg Ser Val Gln Arg Val Ala
 130 135 140

Ser Asp Ala Gly Met Ala Ala Asp Ala Gln Leu Val Ala Ala Arg Asp
 145 150 155 160

Ala Ala Pro Ala Pro Ala Pro Ala Thr Ala Tyr Ala Arg Pro Asp His
 165 170 175

Cys Ala Gly Ala Thr Thr Ala Arg His Asp Glu Leu Ala Arg Arg Gly
 180 185 190

Met Tyr Gly Ala His Ala His Ala Ala Gly Ala Asn Ala Arg Thr Ser
 195 200 205

Gly Glu Arg Gln Leu Val Cys Ala Glu Glu Ile Ser Val Asp Asp Met
 210 215 220

Glu Ile Leu Met
 225

<210> 91

<211> 656

<212> DNA

<213> Brassica rapa subsp. Pekinensis

<220>

<223> G3645 Predicted polypeptide sequence is orthologous to G47

<400> 91

```

cccacgcgtc cgatggatta catcgacaac accgtcgaaa ctcaatcaaa gtacaaaggc      60
atccgtcgcc ggaaatgggg gaaatgggta tcggagattc gagttccggg aactcgcgac      120
cgtctctggt taggctcatt ctccacggcg gaaggcgcag ccgtggcgca cgacgtggct      180
ttctactggt tacaccaacc aaactcgctc gaattcttca acttccctca cttgcttcct      240
ccttccattg tttccaagac ttcgccgagg tctatccagc aagctgcttc taatgccgga      300
atggccggtg acgccggaat cgttaacagc tgtgatcacg cgtcagggaa ctctgggaat      360
ggagatacaa cgacggcgta ttgtgagaat ggaggtgcgt tgaatatatc agtgtatgat      420
tatttggaac gtcacgatca cgtttgaact tcatcttctt gttttttcgt ttaaagatac      480
agctactcaa aagaagcagt gatggagcct ggtgtgtaag caagcaaaac gttgtgaata      540
tatataccgg tatgtttcgc tgttgGCCCA atgcaagaaa cttttgtagt acgaatatat      600
atattttatt ttgaatgcct tcaagaggat tataatgcga gtgaagcttt gtttca      656

```

<210> 92

<211> 144

<212> PRT

<213> Brassica rapa subsp. Pekinensis

<220>

<223> G3645 polypeptide Orthologous to G47

<400> 92

```

Met Asp Tyr Ile Asp Asn Thr Val Glu Thr Gln Ser Lys Tyr Lys Gly
1           5           10           15

```

```

Ile Arg Arg Arg Lys Trp Gly Lys Trp Val Ser Glu Ile Arg Val Pro
20           25           30

```

```

Gly Thr Arg Asp Arg Leu Trp Leu Gly Ser Phe Ser Thr Ala Glu Gly
35           40           45

```

```

Ala Ala Val Ala His Asp Val Ala Phe Tyr Cys Leu His Gln Pro Asn
50           55           60

```

```

Ser Leu Glu Ser Leu Asn Phe Pro His Leu Leu Pro Pro Ser Ile Val
65           70           75           80

```

```

Ser Lys Thr Ser Pro Arg Ser Ile Gln Gln Ala Ala Ser Asn Ala Gly
85           90           95

```

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Met Ala Val Asp Ala Gly Ile Val Asn Ser Cys Asp His Ala Ser Gly
100 105 110

Asn Ser Gly Asn Gly Asp Thr Thr Thr Ala Tyr Cys Glu Asn Gly Gly
115 120 125

Ala Leu Asn Ile Ser Val Tyr Asp Tyr Leu Asp Gly His Asp His Val
130 135 140

<210> 93
<211> 649
<212> DNA
<213> Brassica oleracea

<220>
<223> G3646 Predicted polypeptide sequence is orthologous to G47

<400> 93
cagccgcata acatattact attccccctg gtcatatctt tgacttttat ttttatttgc 60
tctaacctaa aagtattata taagtattgc acaattcata caatcggaat tgactttctt 120
ctcctccaat cgtattttta ttcaacagtt cctctcaaga tcatcaactc aaaaaatgga 180
tcctagagac ggcggagaaa cccatcaggc caagtacaaa ggcacccgtc gccggaaatg 240
gggaanaatgg gtatcggaga ttaggggttcc agcaactcgt gaacgactct ggtaggctc 300
tttctccacc gccgaaggag ctgcggtagc ccacgacgtc gctttttact gcttgcaccg 360
accatcttct ctgcacaacg aagcttttaa cttccctcac ttgctgcaac cttcccttgc 420
ctccaacaca tctcctaagt ccatacaaaa agctgcttcg gacgcaggca tgggcgtaga 480
cgcaggattc gccctaaaca acgacagcgc gagtgggtggc gtggaggaag gcaccgaacg 540
ggaaacgttg aacatctccg tgtacgatta tctagacgac ggtcgcattt gatatttgg 600
tttatatcta cgagcacctt atattagtaa ttaatatagg atgtgaata 649

<210> 94
<211> 138
<212> PRT
<213> Brassica oleracea

<220>
<223> G3646 polypeptide Orthologous to G47

<400> 94

Met Asp Pro Arg Asp Gly Gly Glu Thr His Gln Ala Lys Tyr Lys Gly
1 5 10 15

Ile Arg Arg Arg Lys Trp Gly Lys Trp Val Ser Glu Ile Arg Val Pro
20 25 30

Ala Thr Arg Glu Arg Leu Trp Leu Gly Ser Phe Ser Thr Ala Glu Gly
35 40 45

Ala Ala Val Ala His Asp Val Ala Phe Tyr Cys Leu His Arg Pro Ser
50 55 60

Ser Leu Asp Asn Glu Ala Phe Asn Phe Pro His Leu Leu Gln Pro Ser
65 70 75 80

Leu Ala Ser Asn Thr Ser Pro Lys Ser Ile Gln Lys Ala Ala Ser Asp
85 90 95

Ala Gly Met Gly Val Asp Ala Gly Phe Ala Leu Asn Asn Asp Ser Ala
100 105 110

Ser Gly Gly Val Glu Glu Gly Thr Glu Arg Glu Thr Leu Asn Ile Ser
115 120 125

Val Tyr Asp Tyr Leu Asp Asp Gly Arg Ile
130 135

<210> 95
<211> 495
<212> DNA
<213> Zinnia elegans

<220>
<223> G3647 Predicted polypeptide sequence is orthologous to G47

<400> 95
attcgcggcc gcgaatatga gtaccagctc agatgaaggt aacaactggt taagccaaaa 60
gacttacaaa ggcgtaggt gccgacgatg gggcaaatgg gtgtcagaga ttcgagttcc 120
aggaagtcga gaacggctct ggctaggcac gtactctacg cctgagggtg cagctgtggc 180
tcatgatgta gcctcgtact gtttaaaagg gaatacgtct tttcataaac ttaatatcc 240
gtctatgta cctccgacag cacggacaga cctatctcct aggtccatcc aaaaggctgc 300
gtctgatgct ggtatggcca tagacgcacg gtttatcgcg tctagagata ccacaccgac 360
taatgaggcg ttgaacattt ctgtagatga ttatctttaa attttgagaa ctaatatgt 420
gtcaccaata ttgtaagtcg atctacattg gcaaacacaa tgtacgtgtt tgggtggcact 480
tccagattat tgttt 495

<210> 96
<211> 127
<212> PRT
<213> Zinnia elegans

<220>
<223> G3647 polypeptide Orthologous to G47

<400> 96

MBI0058CIP.ST25.txt

Met Ser Thr Ser Ser Asp Glu Gly Asn Asn Cys Leu Ser Gln Lys Thr
1 5 10 15

Tyr Lys Gly Val Arg Cys Arg Arg Trp Gly Lys Trp Val Ser Glu Ile
20 25 30

Arg Val Pro Gly Ser Arg Glu Arg Leu Trp Leu Gly Thr Tyr Ser Thr
35 40 45

Pro Glu Gly Ala Ala Val Ala His Asp Val Ala Ser Tyr Cys Leu Lys
50 55 60

Gly Asn Thr Ser Phe His Lys Leu Asn Ile Pro Ser Met Leu Pro Pro
65 70 75 80

Thr Ala Arg Thr Asp Leu Ser Pro Arg Ser Ile Gln Lys Ala Ala Ser
85 90 95

Asp Ala Gly Met Ala Ile Asp Ala Arg Phe Ile Ala Ser Arg Asp Thr
100 105 110

Thr Pro Thr Asn Glu Ala Leu Asn Ile Ser Val Asp Asp Tyr Leu
115 120 125

<210> 97
<211> 594
<212> DNA
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3649 Predicted polypeptide sequence is orthologous to G47

<400> 97
atgggcccggg tggcggcgag cggcggcggc ggccggcgag gggagatgat gaggtacagg 60
ggcgtgcggc ggccggcggtg ggggaagtgg gtgtcggaga tccgggtgcc cgggacgcgg 120
gagcgctgt ggctcggctc ctacgccacc gccgaggccg ccgccgtcgc gcacgacgcc 180
gccgtatgcc tctccggct cggcggcggc cgcgcgcgcg ccgcaggcgg aggcggcggg 240
ctcaacttcc ccgccgcgc gctcgcgcgc gcggcgcccg cctcctccta cggcggcgcc 300
ggcgggtctcc tgtccccgcg ctccgtgcag cgcgtggcgt ccgacgccgg catggccgcc 360
gacgcgcagc tcgtggacct gcgccgcgac caccgcgccg ccgccgccgc cgcctcatcc 420
tccggcagcg gcgtggcggg agacggtgca agaaagcaag ggacacgtgg cgaggttagc 480
gacacgtatt ggtgtaggaa tggagaggat gggagcagaa gccggagctc cgggagtgag 540
gagctcattg ttacgaggg cttaagtgt gatgacatgg aaattttgat gtaa 594

<210> 98
<211> 197

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3649 polypeptide Orthologous to G47

<400> 98

Met Gly Arg Val Ala Ala Ser Gly Gly Gly Gly Gly Gly Gly Glu Met
1 5 10 15

Met Arg Tyr Arg Gly Val Arg Arg Arg Arg Trp Gly Lys Trp Val Ser
20 25 30

Glu Ile Arg Val Pro Gly Thr Arg Glu Arg Leu Trp Leu Gly Ser Tyr
35 40 45

Ala Thr Ala Glu Ala Ala Ala Val Ala His Asp Ala Ala Val Cys Leu
50 55 60

Leu Arg Leu Gly Gly Gly Arg Arg Ala Ala Ala Gly Gly Gly Gly Gly
65 70 75 80

Leu Asn Phe Pro Ala Arg Ala Leu Ala Ala Ala Ala Ala Ala Ser Ser
85 90 95

Tyr Gly Gly Ala Gly Gly Leu Leu Ser Pro Arg Ser Val Gln Arg Val
100 105 110

Ala Ser Asp Ala Gly Met Ala Ala Asp Ala Gln Leu Val Asp Leu Arg
115 120 125

Arg Asp His Pro Pro Ala Ala Ala Ala Ala Ser Ser Ser Gly Ser Gly
130 135 140

Val Ala Gly Asp Gly Ala Arg Lys Gln Gly Thr Arg Gly Glu Val Ser
145 150 155 160

Asp Thr Tyr Trp Cys Arg Asn Gly Glu Asp Gly Ser Arg Ser Arg Ser
165 170 175

Ser Gly Ser Glu Glu Leu Ile Val Tyr Glu Gly Leu Ser Val Asp Asp
180 185 190

Met Glu Ile Leu Met
195

<210> 99

<211> 702

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3651 Predicted polypeptide sequence is orthologous to G47

<400> 99

```

atggctgacc tcccatgcat atatatacgc gtagtacgta cacttgcttt cccaacgctc      60
gcgaatcaaaa tcgaggggtga aattaagtca agaacggaga gagatcacgg tgaggttgat      120
ctcagctcgc cggaggaggc aatgagccgg gcggagtgcg gcggcggcga ggaggaggag      180
cgggtgcaggt acagggggcgt gcggcggcgg cgggtggggga agtgggtgtc ggagatccgg      240
gtgcccggca cgcgggagcg gctgtggctg gggtcctacg ccacgccgga ggccgccgcc      300
gtcgcgcacg acacggccgt ctacttcctc cgcgaggaggc cgggcgacgg cgggtggcggc      360
ggcgcgaccg ctcaacttcc cggagcgcgc ggcggccacc gtacggcggc cgccgtggcg      420
cgctgtcgc cgcggtccgt gcagcgcgtg gcgtccgacg cggcatggcc gccgacgcgc      480
agctcggcgt gccgggaccc ggcccggccc gcgccggcga cggcgtagcg gcgcccggat      540
cactgcgccg gcgcgacgac ggcgcggcac gacgagctgg cgcgccgcgg gatgtacggc      600
gctcacgcgc atgccgccgg cggaacgcc aggacgagcg gcgagcggca gctcgtctgt      660
gccgaggaga ttagcgtgga tgacatggag atcctgatgt aa                          702

```

<210> 100

<211> 233

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3651 polypeptide Orthologous to G47

<400> 100

```

Met Ala Asp Leu Pro Cys Ile Tyr Ile Arg Val Val Arg Thr Leu Ala
1           5           10           15

```

```

Phe Pro Thr Leu Ala Asn Gln Ile Glu Gly Glu Ile Lys Ser Arg Thr
          20           25           30

```

```

Glu Arg Asp His Gly Glu Val Asp Leu Ser Ser Pro Glu Glu Ala Met
          35           40           45

```

```

Ser Arg Ala Glu Cys Gly Gly Gly Glu Glu Glu Glu Arg Cys Arg Tyr
          50           55           60

```

```

Arg Gly Val Arg Arg Arg Arg Trp Gly Lys Trp Val Ser Glu Ile Arg
          65           70           75           80

```

```

Val Pro Gly Thr Arg Glu Arg Leu Trp Leu Gly Ser Tyr Ala Thr Pro
          85           90           95

```

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Glu Ala Ala Val Ala His Asp Thr Ala Val Tyr Phe Leu Arg Gly
100 105 110

Gly Ala Gly Asp Gly Gly Gly Gly Ala Thr Ala Gln Leu Pro Gly
115 120 125

Ala Arg Gly Gly His Arg Thr Ala Ala Ala Val Ala Arg Leu Ser Pro
130 135 140

Arg Ser Val Gln Arg Val Ala Ser Asp Ala Ala Trp Pro Pro Thr Arg
145 150 155 160

Ser Ser Ala Cys Arg Asp Pro Ala Arg Pro Ala Pro Ala Thr Ala Tyr
165 170 175

Ala Arg Pro Asp His Cys Ala Gly Ala Thr Thr Ala Arg His Asp Glu
180 185 190

Leu Ala Arg Arg Gly Met Tyr Gly Ala His Ala His Ala Ala Gly Ala
195 200 205

Asn Ala Arg Thr Ser Gly Glu Arg Gln Leu Val Cys Ala Glu Glu Ile
210 215 220

Ser Val Asp Asp Met Glu Ile Leu Met
225 230

<210> 101
<211> 855
<212> DNA
<213> Lotus corniculatus var. japonicus

<220>
<223> G3663 Predicted polypeptide sequence is orthologous to G2999

<400> 101
atggaaatga gagagatgcc ttccactttg atatataatc tccccaacag agattcctct 60
tctccatctc taccttcaag tagtgatcag ccttctcaaa ctcacacaat aatcttcaat 120
catccaccta aactttctca taaccaccac catcatattt atacccttc ttctacttct 180
cctcctcttc caccaaactc agttcaactt caacaacaac ccacaagaga tccagatcca 240
agttcttctt cttctctatt aattagatac agagaatgcc tgaggaacca tgcagcgaga 300
ttagggagtc atgtcacaga tggatgtggc gagttcatgc caaatggaga acaaggaacc 360
ccagaatcat tgatctgtgc tgcttgcgag tgccaccgca attttcacag aaaagaggct 420
caaggagaac ctcaacaagt ttccaactat catcacaca aaagcaatgg tcagaacagg 480
attcaccctt cttctctgca tcataaacat ggattttctt cgtcaccagg gttgatgatg 540
ggctttgggg gaggcagtgg aggccttgca gctgaatcct caagtgaaga tctcaacatg 600

MBI0058CIP.ST25.txt

```

tttcaccagt ccaatgatgg aggccaatta tcagtgcagc caccactatc atcaaagaag 660
aggttcagaa ctaagttcac ccagcaacaa aaggacagga tgatggagtt tgctgagaaa 720
ctgggggtgga agatccagaa gcaagatgaa gaggaagtga agcaattctg ctctcatggt 780
gggtgtaaaaa gacaggcttt caaggtttgg atgcacaata gcaagcaagc aatgaagaag 840
aagcaaatca tgtaa 855

```

```

<210> 102
<211> 284
<212> PRT
<213> Lotus corniculatus var. japonicus

```

```

<220>
<223> G3663 polypeptide Orthologous to G2999

```

```

<400> 102

```

```

Met Glu Met Arg Glu Met Pro Ser Thr Leu Ile Tyr Asn Leu Pro Asn
1 5 10 15

```

```

Arg Asp Ser Ser Ser Pro Ser Leu Pro Ser Ser Ser Asp Gln Pro Ser
20 25 30

```

```

Gln Thr His Thr Ile Ile Phe Asn His Pro Pro Lys Leu Ser His Asn
35 40 45

```

```

His His His His Ile Tyr Thr Pro Ser Ser Thr Ser Pro Pro Leu Pro
50 55 60

```

```

Pro Asn Ser Val Gln Leu Gln Gln Gln Pro Thr Arg Asp Pro Asp Pro
65 70 75 80

```

```

Ser Ser Ser Ser Ser Leu Leu Ile Arg Tyr Arg Glu Cys Leu Arg Asn
85 90 95

```

```

His Ala Ala Arg Leu Gly Ser His Val Thr Asp Gly Cys Gly Glu Phe
100 105 110

```

```

Met Pro Asn Gly Glu Gln Gly Thr Pro Glu Ser Leu Ile Cys Ala Ala
115 120 125

```

```

Cys Glu Cys His Arg Asn Phe His Arg Lys Glu Ala Gln Gly Glu Pro
130 135 140

```

```

Gln Gln Val Ser Asn Tyr His His Asn Lys Ser Asn Gly Gln Asn Arg
145 150 155 160

```

```

Ile His Pro Ser Ser Leu His His Lys His Gly Phe Ser Ser Ser Pro
165 170 175

```

Gly Leu Met Met Gly Phe Gly Gly Gly Ser Gly Gly Pro Ala Ala Glu
180 185 190

Ser Ser Ser Glu Asp Leu Asn Met Phe His Gln Ser Asn Asp Gly Gly
195 200 205

Gln Leu Ser Val Gln Pro Pro Leu Ser Ser Lys Lys Arg Phe Arg Thr
210 215 220

Lys Phe Thr Gln Gln Gln Lys Asp Arg Met Met Glu Phe Ala Glu Lys
225 230 235 240

Leu Gly Trp Lys Ile Gln Lys Gln Asp Glu Glu Glu Val Lys Gln Phe
245 250 255

Cys Ser His Val Gly Val Lys Arg Gln Ala Phe Lys Val Trp Met His
260 265 270

Asn Ser Lys Gln Ala Met Lys Lys Lys Gln Ile Met
275 280

<210> 103
<211> 1162
<212> DNA
<213> Flaveria bidentis

<220>
<223> G3668 Predicted polypeptide sequence is orthologous to G2999

<400> 103
gtttttttttt tttttttttt tttttttttt tttgtcaaag cagaacagaa ttgcatacgt 60
aggtaacatt gcatacactt gcacactcta aacacacact tttgctttat tttttttttt 120
tgcaggcgat ggggttaattc atgtccacac cctcttcttt cacttatcct ctgatcaacc 180
tcacatcacc caccattgcc tctccatctt attcaccatc attcatccta atctgtttct 240
taattcacct ctggttggtta atcacatcgg agcttataat tactaatgg agtttgatga 300
acacgatgag caggaagagg aggtcggaat tcagctcact ccggggagtt ttgacgccgt 360
cgggactcc ggccggagga aatccggtgg cggtggcggt ggcggtggat acaggtataa 420
ggaatgtttg aagaaccacg cggtaggcat tggcggtcag gcggtggacg gatgtggaga 480
gtttatggct gccggagatg aaggtaacct agatgcacta aagtgcgccg cgtgcaattg 540
tcaccggaac ttccatcgga aggaggtgga gggacaacaa cggcagcatc aacaccagca 600
gcaagctgcg ttacagcacc agtatatcac cgcgacgccg tactaccacc accaccaccg 660
gccgacggga tacctgcaca tgaaaccgcc tccgtcgtcg ctccaccagc ggcagctggc 720
tctcccgtcg acgtctcgag atgatctgga tgagatctca aaccctagct ccagcggtgg 780

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cggtggcggtt ggtggaagcg gttcgaagaa gagattccga acgaaattca cacaggatca 840
gaaggatcgg atgctggcgt tctcggaggc gttaggggtgg cgtattcaga agcacgatga 900
ggccgccgtg caacaattct gcaacgaaac cggcggttaa cggcacgttc ttaaggtctg 960
gatgcacaat aataagcaca caatcggtaa gaaaccctaa ttttgcaaca aaaacgaaca 1020
agctacagaa attattaatg gaatctcatt cgtaggatcg atttcagtgt cgtttaggta 1080
gtatttttgt ttgatttcta tcgttgatgat cgtagtctct taatttaact cgatctgaat 1140
gttgattaat cgtttgattt cc 1162

<210> 104
<211> 237
<212> PRT
<213> Flaveria bidentis

<220>
<223> G3668 polypeptide Orthologous to G2999

<400> 104

Met Glu Phe Asp Glu His Asp Glu Gln Glu Glu Glu Val Gly Ile Gln
1 5 10 15

Leu Thr Pro Gly Ser Phe Asp Ala Val Gly Asn Ser Gly Arg Arg Lys
20 25 30

Ser Gly Gly Gly Gly Gly Gly Gly Gly Tyr Arg Tyr Lys Glu Cys Leu
35 40 45

Lys Asn His Ala Val Gly Ile Gly Gly Gln Ala Val Asp Gly Cys Gly
50 55 60

Glu Phe Met Ala Ala Gly Asp Glu Gly Thr Leu Asp Ala Leu Lys Cys
65 70 75 80

Ala Ala Cys Asn Cys His Arg Asn Phe His Arg Lys Glu Val Glu Gly
85 90 95

Gln Gln Arg Gln His Gln His Gln Gln Gln Ala Ala Leu Gln His Gln
100 105 110

Tyr Ile Thr Ala Thr Pro Tyr Tyr His His His His Arg Pro Thr Gly
115 120 125

Tyr Leu His Met Lys Pro Pro Pro Ser Ser Leu His Gln Arg Gln Leu
130 135 140

Ala Leu Pro Ser Thr Ser Arg Asp Asp Leu Asp Glu Ile Ser Asn Pro
145 150 155 160

MBI0058CIP.ST25.txt

Ser Ser Ser Gly Gly Gly Gly Val Gly Gly Ser Gly Ser Lys Lys Arg
165 170 175

Phe Arg Thr Lys Phe Thr Gln Asp Gln Lys Asp Arg Met Leu Ala Phe
180 185 190

Ser Glu Ala Leu Gly Trp Arg Ile Gln Lys His Asp Glu Ala Ala Val
195 200 205

Gln Gln Phe Cys Asn Glu Thr Gly Val Lys Arg His Val Leu Lys Val
210 215 220

Trp Met His Asn Asn Lys His Thr Ile Gly Lys Lys Pro
225 230 235

<210> 105
<211> 813
<212> DNA
<213> Lotus corniculatus var. japonicus

<220>
<223> G3670 Predicted polypeptide sequence is orthologous to G2999

<400> 105
atggagtttg atgagcaaga agagcaagat gaagaaatgg ggatcccgga gtcaccgccg 60
ccggtgccgg cgagttacga cccgcttttg aactcagcac cgagatccaa aatcgagag 120
gtttcagcgc ctgtaatcgg gaggaaggc ggctcgttta ccccgccggg ggcagcgggg 180
gttgtagagt acagggaatg ccagaagaac cacgccgtca gcttcggcgg ccacgccgtc 240
gacgggtgct gcgagttcat ggctgccgga gatgaaggca cgctggaggc tgtgatctgc 300
gccgcctgta actgtcaccg gaacttccac cgcaaggaga tcgacggcga aacagtggcc 360
tcgtgccaga ggcagcagcc tccgcctcct ccggtgcacc accaccagta ccacagccaa 420
ttctcccctt actaccaccg tggacctcag caccatgccg cctccggcgg ctacctccac 480
caccacctga caacatctcc gacggcgccc caccggccgt tagcacttcc accggcgact 540
tcaggagggtg gattcagcag ggaggaggaa gacatgtcta accctagcag cagtgggtgga 600
ggcggcgagg gtggaatgaa aaagaggtac aggaccaagt tcacgccgga gcagaaggag 660
aagatgctgg cttttgcaga agagcttggt tggagaatcc agaagcatca agaagctgct 720
gttgaacaat tctgtgctga aacttggtgtg aggagaaacg ttctcaaggt ttggatgcac 780
aataacaaga acacgcttgg taagaaaccc taa 813

<210> 106
<211> 270
<212> PRT
<213> Lotus corniculatus var. japonicus

<220>

<223> G3670 polypeptide Orthologous to G2999

<400> 106

```

Met Glu Phe Asp Glu Gln Glu Glu Gln Asp Glu Glu Met Gly Ile Pro
1          5          10          15

Glu Ser Pro Pro Pro Val Pro Ala Ser Tyr Asp Pro Leu Leu Asn Ser
          20          25          30

Ala Pro Arg Ser Lys Ile Ala Glu Val Ser Ala Pro Val Ile Gly Arg
          35          40          45

Lys Gly Gly Ser Phe Thr Pro Pro Val Ala Ala Gly Val Val Arg Tyr
50          55          60

Arg Glu Cys Gln Lys Asn His Ala Val Ser Phe Gly Gly His Ala Val
65          70          75          80

Asp Gly Cys Cys Glu Phe Met Ala Ala Gly Asp Glu Gly Thr Leu Glu
          85          90          95

Ala Val Ile Cys Ala Ala Cys Asn Cys His Arg Asn Phe His Arg Lys
          100          105          110

Glu Ile Asp Gly Glu Thr Val Ala Ser Cys Gln Arg Gln Gln Pro Pro
          115          120          125

Pro Pro Pro Val His His His Gln Tyr His Ser Gln Phe Ser Pro Tyr
          130          135          140

Tyr His Arg Gly Pro Gln His His Ala Ala Ser Gly Gly Tyr Leu His
145          150          155          160

His His Leu Thr Thr Ser Pro Thr Ala Pro His Arg Pro Leu Ala Leu
          165          170          175

Pro Pro Ala Thr Ser Gly Gly Gly Phe Ser Arg Glu Glu Glu Asp Met
          180          185          190

Ser Asn Pro Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly Met Lys Lys
          195          200          205

Arg Tyr Arg Thr Lys Phe Thr Pro Glu Gln Lys Glu Lys Met Leu Ala
          210          215          220

Phe Ala Glu Glu Leu Gly Trp Arg Ile Gln Lys His Gln Glu Ala Ala
225          230          235          240

```


Val Glu Gln Phe Cys Ala Glu Thr Cys Val Arg Arg Asn Val Leu Lys
 245 250 255

Val Trp Met His Asn Asn Lys Asn Thr Leu Gly Lys Lys Pro
 260 265 270

<210> 107
 <211> 1169
 <212> DNA
 <213> Oryza sativa (japonica cultivar-group)

<220>
 <223> G3671 Predicted polypeptide sequence is orthologous to G2999

<400> 107
 aagtgttttc ctagctaggt agctagctag ctagacgagc ttgccggccg gccggccggc 60
 gacggcgacc atggacttcg atgaccatga cgacggcgac gaggagatgc cgccgatgcc 120
 ggtgagctcg agctacgaga ctccgccgca gcatggcctt gccggcggtg ggatggcgcc 180
 caagcctcct ggtgagattg gcagccgtgt gaagggcccc agctgcggtg gcggcaggta 240
 ccgcgagtg ctcagaacc acgcggttg catcgccggc caccgctgg acggctgcgg 300
 cgagttcatg gcggccggcg aggagggcac catcgacgcg ctccgctgcg ccgcgtgcaa 360
 ctgccaccgc aacttcacc ggaaggagtc cgagtcgctt gccggcgagg gctcgccctt 420
 ctccccggcc gccgtcgtcc cctacggcgc caccgcccac caccagttct cccgtacta 480
 ccgcacccct gccggttacc tccaccacca ccagcaccac atggccgcgg cagccgcggc 540
 cgccgcggcc gcagccggcg gctaccgcga gcggccccct gcgctcccgt ccacctcca 600
 cagcggccgc gacgacggcg acgacctgtc cgggatggtg gggcccatgt cggcggtggg 660
 gccgctcagc ggcattgccc tcggcgccgg cccgtccggc tccggctccg gcaagaagcg 720
 gttccgcacc aagttcacc aggagcagaa ggacaagatg ctggcgttcg ccgagcgct 780
 cgggtggcgc atccagaagc acgacgagc cgccgtgcag cagttctgtg acgaggtcgg 840
 cgtcaagcgc cagtgctca aggtgtggat gcacaacaac aagcacacc tgggcaagaa 900
 gctgccatga ccgggagcaa atgcatttga tctcatcgtc ggcattgatg accaagttgt 960
 gggacgacgc atgcatccat gtccatccca agctagctga gctgatcgac cggccgtggc 1020
 ttagccaccc ggaccccggt atggtaggta cctgaacctt atttatttag agttggactt 1080
 aattaattgg tggcttaggt taatctgtag caagagagac tgagagagca ttcgttctcg 1140
 gctctagtag gtggttcttt cttcttttc 1169

<210> 108
 <211> 264
 <212> PRT
 <213> Oryza sativa (japonica cultivar-group)

MBI0058CIP.ST25.txt

<220>

<223> G3671 polypeptide Orthologous to G2999

<400> 108

Met Pro Val Ser Ser Ser Tyr Glu Thr Pro Pro Gln His Gly Leu Ala
1 5 10 15

Gly Gly Gly Met Ala Pro Lys Pro Pro Gly Glu Ile Gly Ser Arg Val
20 25 30

Lys Gly Pro Ser Cys Gly Gly Gly Arg Tyr Arg Glu Cys Leu Lys Asn
35 40 45

His Ala Val Gly Ile Gly Gly His Ala Val Asp Gly Cys Gly Glu Phe
50 55 60

Met Ala Ala Gly Glu Glu Gly Thr Ile Asp Ala Leu Arg Cys Ala Ala
65 70 75 80

Cys Asn Cys His Arg Asn Phe His Arg Lys Glu Ser Glu Ser Leu Ala
85 90 95

Gly Glu Gly Ser Pro Phe Ser Pro Ala Ala Val Val Pro Tyr Gly Ala
100 105 110

Thr Pro His His Gln Phe Ser Pro Tyr Tyr Arg Thr Pro Ala Gly Tyr
115 120 125

Leu His His His Gln His His Met Ala Ala Ala Ala Ala Ala Ala Ala
130 135 140

Ala Ala Ala Gly Gly Tyr Pro Gln Arg Pro Leu Ala Leu Pro Ser Thr
145 150 155 160

Ser His Ser Gly Arg Asp Asp Gly Asp Asp Leu Ser Gly Met Val Gly
165 170 175

Pro Met Ser Ala Val Gly Pro Leu Ser Gly Met Ser Leu Gly Ala Gly
180 185 190

Pro Ser Gly Ser Gly Ser Gly Lys Lys Arg Phe Arg Thr Lys Phe Thr
195 200 205

Gln Glu Gln Lys Asp Lys Met Leu Ala Phe Ala Glu Arg Val Gly Trp
210 215 220

Arg Ile Gln Lys His Asp Glu Ala Ala Val Gln Gln Phe Cys Asp Glu
225 230 235 240

Val Gly Val Lys Arg His Val Leu Lys Val Trp Met His Asn Asn Lys
 245 250 255

His Thr Leu Gly Lys Lys Leu Pro
 260

<210> 109
 <211> 1891
 <212> DNA
 <213> Oryza sativa (indica cultivar-group)

<220>
 <223> G3674 Predicted polypeptide sequence is orthologous to G2999

<400> 109
 aagcttttct taagctcgcc aagaacacac ccgagaaatc caaaagggag ggaaaagaaa 60
 ggggggtggcc ggccggtcgg tcggtcggcg gccatggatt tcgacgacca tgacgagggt 120
 gacggcgacg aggagatgcc tccgatgcct ctgagctcgg gctacgacgc gccgatgcag 180
 cccgggcttg gaggtggcgg tggcgggggtg cccaagccgg gaggtggagt cggcggcggc 240
 ggtggtggtg gtggtggtgg tggaggagga ggggcgagggt atcgggagtg cctcaagaac 300
 cacgccgtcg gcatcggcgg gcacgccgtg gacggctcgg gcgagttcat ggcttcgggc 360
 gaggaggggt ccatcgacgc gctccgctgc gccgcctcgg gctgccaccg taacttcac 420
 cgcaaggagt cggagtcccc cacgggcgtc gggccggccg agccttcgc cgtgtcccc 480
 gccgccatct cggcctacgg cgctcggcg caccaccagt tctcccccta ctaccgcacc 540
 ccggcagggg acctccacca ccagcagcac cagatggcgg ccgcggcggc ggccgcggcc 600
 gccgccgcag cgggcgggcta cccgcagcgg cccctcgcgc tgccgtccac ctcccactcg 660
 ggacgcgacg agggcgacga catgtccggg atggtcggcc ccatggtgat tggcccatg 720
 gtcggcatgt ccctcggctc cgccggcccc tccggtcgcg gctccggcaa gaagcggttc 780
 cgcacaaagt tcacgcagga gcagaaggac aagatgctcg ccttcgcgga gcggctcggg 840
 tggcgcaccc agaagcacga cgaggccgcc gtgcagcagt tctgcgagga ggtctgcgtc 900
 aagcgccatg tcctcaaggt ttggatgcac aacaacaagc acaccctggg caagaaggcg 960
 ccatagctaa gctaagccaa gcaagctcag ctgagctcat ctctcccgg tgctaggtac 1020
 ctgcactgca actgcaactg catgcacac catctccatc tacttctact acctccttac 1080
 ccgcggctaa ttagcctttt tctttgcctt cttttacctc acctgagtag aagcttagct 1140
 aggttcgtag cgagcaagct gttcttggtg gttttagggg aggtggtggt tgctgctgct 1200
 gctgcttttg catccttcct tgtttctttt tcgttatattt attccattgt ggttgggttc 1260
 tttgggcttg tggttgccgt cgttgttggt tcctagtaga tgatgacgac gacgtttggt 1320
 gttgggaagg aagaggacat ggatggcgat ttgccgatcg atttagatct tgggaatgta 1380

MBI0058CIP.ST25.txt

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gtacttttgt gttgcaattg aaatttcctt cctggggatt tgggttgctg cacggtttgt 1440
ttgtttcatc atttcttttc ccctatatatt cttgtgcttg gcacttcatc atcagtagca 1500
cttgtagttc gtctagctaa caactagggc agataaagat tcagaaaggt cggctgcaac 1560
tatatgagct gcaacactgt tgcattcaca tcgatctccc tcgcttccaa tttccagacc 1620
tgggcaccaa cttgtccatg atccgtccgc ttcacctgtc tactctgaaa ttccaatttc 1680
tctagctacc atgttcgctg catttttctt ccgagttctc gatctcactg tatccgctgc 1740
atttactcgt cttccacatc tcgcgagcag tgatgccgca ttgctgcca tgtgttagga 1800
cgcagagctt gcagaagcta tagcaatggc cggggacttt ttagaattta gtctatgtga 1860
attcaatgaa gcctcgtcct ctcttttact c 1891

```

<210> 110

<211> 290

<212> PRT

<213> Oryza sativa (indica cultivar-group)

<220>

<223> G3674 polypeptide Orthologous to G2999

<400> 110

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Met Asp Phe Asp Asp His Asp Glu Gly Asp Gly Asp Glu Glu Met Pro
1          5          10          15

Pro Met Pro Leu Ser Ser Gly Tyr Asp Ala Pro Met Gln Pro Gly Leu
          20          25          30

Gly Gly Gly Gly Gly Gly Val Pro Lys Pro Gly Gly Gly Val Gly Gly
          35          40          45

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Arg Tyr Arg
          50          55          60

Glu Cys Leu Lys Asn His Ala Val Gly Ile Gly Gly His Ala Val Asp
65          70          75          80

Gly Cys Gly Glu Phe Met Ala Ser Gly Glu Glu Gly Ser Ile Asp Ala
          85          90          95

Leu Arg Cys Ala Ala Cys Gly Cys His Arg Asn Phe His Arg Lys Glu
          100          105          110

Ser Glu Ser Pro Thr Gly Val Gly Pro Ala Glu Pro Ser Ala Val Ser
          115          120          125

Pro Ala Ala Ile Ser Ala Tyr Gly Ala Ser Pro His His Gln Phe Ser
          130          135          140

```

MBI0058CIP.ST25.txt

Pro Tyr Tyr Arg Thr Pro Ala Gly Tyr Leu His His Gln Gln His Gln
145 150 155 160

Met Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Gly Gly Tyr
165 170 175

Pro Gln Arg Pro Leu Ala Leu Pro Ser Thr Ser His Ser Gly Arg Asp
180 185 190

Glu Gly Asp Asp Met Ser Gly Met Val Gly Pro Met Val Ile Gly Pro
195 200 205

Met Val Gly Met Ser Leu Gly Ser Ala Gly Pro Ser Gly Ser Gly Ser
210 215 220

Gly Lys Lys Arg Phe Arg Thr Lys Phe Thr Gln Glu Gln Lys Asp Lys
225 230 235 240

Met Leu Ala Phe Ala Glu Arg Leu Gly Trp Arg Ile Gln Lys His Asp
245 250 255

Glu Ala Ala Val Gln Gln Phe Cys Glu Glu Val Cys Val Lys Arg His
260 265 270

Val Leu Lys Val Trp Met His Asn Asn Lys His Thr Leu Gly Lys Lys
275 280 285

Ala Pro
290

<210> 111
<211> 789
<212> DNA
<213> Brassica napus

<220>
<223> G3675 Predicted polypeptide sequence is orthologous to G2999

<400> 111
ggtgacgttg aaggattaaa aataaagagg gacagagaga gagagagata agaaaaatgg 60
actttgagga gcaagaagaa gaaatggaga tgtcaggtgc taaccccacc ggaggttacg 120
actctctgag cggcgagggg gcgacctcaa gcggaggtgg tggcggagga ggtagtagaa 180
aaaccgttgg agggtcgaag gtaaggtaca gagagtgctt aaaaaatcat gccgttaaca 240
tcggcggcca cgccgtggac ggctgctgtg agttcatgcc ttccggtgaa gatggttcac 300
tcgacgctct caagtgtgca gcttgtggct gccaccgcaa cttccaccgg aaggaaaccg 360
aagtcatgag cggcagggca cacagggttc caacgtacta caaccgtcct cctcagctgc 420

MBI0058CIP.ST25.txt

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cgccgccagg atacctccat ttaacgtctc cggcggcggc aggacagcct tacaagcctc 480
ctgcggcctc tggggacgag gaggatacgt cgaatccgag cagcagcggc ggaacaaggg 540
ctaagaggtt tagaacgaag ttcacggcgg agcagaagga taagatgttg gccttcgcgg 600
agaggttggg ttggagaatt cagaagcatg atgacgcggc ggttgagcag ttctgtgcgg 660
aaactggtgt taggagacaa gtgcttaaga tttggatgca taacaacaag aactctctgg 720
gtaggaaacc ctaaaatttc ttgtatgatt taagcgcaag agatcatcat tgctcctttt 780
tcttttttgg 789
```

<210> 112
 <211> 225
 <212> PRT
 <213> Brassica napus

<220>
 <223> G3675 polypeptide Orthologous to G2999

<400> 112

Met Asp Phe Glu Glu Gln Glu Glu Glu Met Glu Met Ser Gly Ala Asn
 1 5 10 15

Pro Thr Gly Gly Tyr Asp Ser Leu Ser Gly Glu Gly Ala Thr Ser Ser
 20 25 30

Gly Gly Gly Gly Gly Gly Gly Ser Arg Lys Thr Val Gly Gly Ser Lys
 35 40 45

Val Arg Tyr Arg Glu Cys Leu Lys Asn His Ala Val Asn Ile Gly Gly
 50 55 60

His Ala Val Asp Gly Cys Cys Glu Phe Met Pro Ser Gly Glu Asp Gly
 65 70 75 80

Ser Leu Asp Ala Leu Lys Cys Ala Ala Cys Gly Cys His Arg Asn Phe
 85 90 95

His Arg Lys Glu Thr Glu Val Met Ser Gly Arg Ala His Arg Val Pro
 100 105 110

Thr Tyr Tyr Asn Arg Pro Pro Gln Leu Pro Pro Pro Gly Tyr Leu His
 115 120 125

Leu Thr Ser Pro Ala Ala Ala Gly Gln Pro Tyr Lys Pro Pro Ala Ala
 130 135 140

Ser Gly Asp Glu Glu Asp Thr Ser Asn Pro Ser Ser Ser Gly Gly Thr
 145 150 155 160

Arg Ala Lys Arg Phe Arg Thr Lys Phe Thr Ala Glu Gln Lys Asp Lys
165 170 175

Met Leu Ala Phe Ala Glu Arg Leu Gly Trp Arg Ile Gln Lys His Asp
180 185 190

Asp Ala Ala Val Glu Gln Phe Cys Ala Glu Thr Gly Val Arg Arg Gln
195 200 205

Val Leu Lys Ile Trp Met His Asn Asn Lys Asn Ser Leu Gly Arg Lys
210 215 220

Pro
225

<210> 113
<211> 1529
<212> DNA
<213> Zea mays

<220>
<223> G3680 Predicted polypeptide sequence is orthologous to G2999

<400> 113
ctcgaaggcg gccgggctct ggccggggccc tgaccgcgtcg tcccatgcta aaagcccagg 60
gttaggagct agaggtaatc tctctcccc gcggccactc cccagtgggc gtggggggcgc 120
cgcatggaag ccatggacgt caagtacaag cccgtcatgt tccccaacgg cgccggcctc 180
aagaagccga agccggcggc ggccgtggcg ctggccgggg agccgctgta ccgggagtg 240
ctcaagaacc acgccgcgag cctggggcggg cacgccgtcg acggttgcg cgagttcatg 300
ccctcgccgg gggccaaccc cgccgacccg acgtcgctca agtgcgcggc gtgcggggtgc 360
caccgcaact tccaccgccg gacgttgag ggttccccctc cgccgcccgc gcccgcccg 420
ctggcgctcc cgcctccgcc gagcgtgatg cacggccagc cgcaccgcgc ccgggaggag 480
acgcccggag accgccaccc gggggtcgtc gacgccgacg actccgattc cgactcgga 540
ggctcggagt acgacgagga gcggtcggtg tccccgccgc cgccgcccga ccacctgctg 600
ccggcgccgg tggcgagca gccccgcc cgcgtcact tcccgacggc gccgcacatg 660
gtgctctcgc tcggttcgg cgtgcccggg cccgcggtgg cggtatcccc ggcgcagagg 720
ctggccccga cccagctgac gccgtccagc gcgccgcccc acgccggggg cgcgatgccc 780
atgcccagga agcggttccg caccaagttc accgccgagc agaagcagcg gatgcaggag 840
ctgtcggagc ggctcgggtg gcggtgcag aagcgcgacg aggccatcgt cgacgagtg 900
tgccgcgaca tcggcgctcg caagggcgctc ttcaaggtct ggatgcacaa caacaagcac 960
aacttcctgg gcgggcacag cgcccgccgc agcgcctcct cgcccgcccc cgccccgcc 1020

MBI0058CIP.ST25.txt

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gccgcgtcgc tccaaacccc agccgccggc gccggcgccg gcgctgctgc agcacctca 1080
ttcaaccctt ccaggatcac cctccccct cccgtcctca cctcgtcccc gacggccgcc 1140
accggcttca acatcaacgg cgccgcctcc tcggcgccca ccgtcgccac cgactacacc 1200
acggacaacg ccaacggagc ttcgtcgccg cactccgctt gaactagaga agggagaaga 1260
gaggaggggg aaggggaagg agagcggaga gggagagaaa catgtagctt aatttcagt 1320
atcactcgtt ttttttttgt ttagacctct tgccatctac taagaaatta accccaagaa 1380
aaagcatgcc gctgtgccc atgcctagaa aacaaaaaaa aaaaaacaaa aaaaaaaaaa 1440
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1529

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<210> 114
 <211> 372
 <212> PRT
 <213> Zea mays

<220>
 <223> G3680 polypeptide Orthologous to G2999

<400> 114

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Met Glu Ala Met Asp Val Lys Tyr Lys Pro Val Met Phe Pro Asn Gly
1          5          10          15

Ala Gly Leu Lys Lys Pro Lys Pro Ala Ala Ala Val Ala Leu Ala Gly
          20          25          30

Glu Pro Leu Tyr Arg Glu Cys Leu Lys Asn His Ala Ala Ser Leu Gly
          35          40          45

Gly His Ala Val Asp Gly Cys Gly Glu Phe Met Pro Ser Pro Gly Ala
          50          55          60

Asn Pro Ala Asp Pro Thr Ser Leu Lys Cys Ala Ala Cys Gly Cys His
65          70          75          80

Arg Asn Phe His Arg Arg Thr Leu Glu Gly Ser Pro Pro Pro Pro Ala
          85          90          95

Pro Ala Pro Leu Ala Leu Pro Pro Pro Pro Ser Val Met His Gly Gln
          100          105          110

Pro His Arg Ala Arg Glu Glu Thr Pro Glu Asp Arg His Pro Gly Val
          115          120          125

Val Asp Ala Asp Asp Ser Asp Ser Asp Ser Glu Gly Ser Glu Tyr Asp
          130          135          140

```


Glu Glu Arg Ser Val Ser Pro Pro Pro Pro Pro His His Leu Leu Pro
145 150 155 160

Ala Pro Val Ala Gln Gln Pro Pro Pro Pro Ser Tyr Phe Pro Thr Ala
165 170 175

Pro His Met Val Leu Ser Leu Gly Ser Gly Val Pro Gly Pro Ala Val
180 185 190

Ala Val Ser Pro Ala Gln Arg Leu Ala Pro Thr Gln Leu Thr Pro Ser
195 200 205

Ser Ala Pro Pro His Ala Gly Gly Ala Met Pro Met Pro Arg Lys Arg
210 215 220

Phe Arg Thr Lys Phe Thr Ala Glu Gln Lys Gln Arg Met Gln Glu Leu
225 230 235 240

Ser Glu Arg Leu Gly Trp Arg Leu Gln Lys Arg Asp Glu Ala Ile Val
245 250 255

Asp Glu Trp Cys Arg Asp Ile Gly Val Gly Lys Gly Val Phe Lys Val
260 265 270

Trp Met His Asn Asn Lys His Asn Phe Leu Gly Gly His Ser Ala Arg
275 280 285

Arg Ser Ala Ser Ser Pro Ala Pro Ala Pro Ala Ala Ala Ser Leu Gln
290 295 300

Thr Pro Ala Ala Gly Ala Gly Ala Gly Ala Ala Ala Ala Pro Ser Phe
305 310 315 320

Asn Pro Ser Arg Ile Thr Pro Pro Pro Pro Val Leu Thr Ser Ser Pro
325 330 335

Thr Ala Ala Thr Gly Phe Asn Ile Asn Gly Ala Ala Ser Ser Ala Pro
340 345 350

Thr Val Ala Thr Asp Tyr Thr Thr Asp Asn Ala Asn Gly Ala Ser Ser
355 360 365

Pro His Ser Ala
370

<210> 115
<211> 990

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3683 Predicted polypeptide sequence is orthologous to G2999

<400> 115

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atggatcttt ctggggcgca gggcgagctg ccgttgccaa tgcacgccgc ggcgtcgccg      60
tacctcggct tgcaccatga ccaccaccac catcatggcg gcggcgggcg cggaggaggg      120
atgaatgggc ggcacatgtc gccgccgacg ccaccggcgg cggcgaggga gtcgaaggcg      180
gtggtggtgg tgtcgtcgtc ggcgacggcg gcggcgaggt acagggagtg cctcaagaac      240
cacgcggcgg ccatcggcgg cagcgccacg gacgggtgcg gcgagttcat gcccgcgggc      300
gaggaaggct cgctcgacgc gctccgctgc tccgcctgcg gctgccaccg caacttcac      360
cgcaaggagc tcgacgccgc cgccgccccg ccgctccacc accaccacca ccaactgctc      420
ggcgtcgggc cgcacccccg cggccacggc caccaccacc accacctcct ggtggcgggc      480
ctgccgccgc cgacgcggat ggtgatgccg ctgagcgcca tgcacacgtc ggagtcggac      540
gacgcgcggc cgcgccccg cggcgggcgg gcggcgagga agcggttccg gaccaagttc      600
acggcgggagc agaaggcgcg gatgctgggg ttccgcgagg aggtcgggtg gcggctgcag      660
aagctggagg acgccgtcgt gcagcgcttc tgccaggagg tcggcgtaaa gcgccgcgtc      720
ctcaaggctt ggatgcacaa caacaagcac accctcgccc gccgccacct ccacctctcc      780
cccgccgccg ccgccggaga cgacgacgac gacggcgcgc cgccgccgca ccccgacccc      840
cggcgggcgg agctcgccgc cgccgccgca ccacctccgg ctccagtaac ccaacacatc      900
aagaaatccg ttgacaacaa aagcctcatt tctagcttag ctgcattgca ttgcattgct      960
ctactactgt tccatcaaat tgatgcttaa      990

```

<210> 116

<211> 329

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3683 polypeptide Orthologous to G2999

<400> 116

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Met Asp Leu Ser Gly Ala Gln Gly Glu Leu Pro Leu Pro Met His Ala
1          5          10          15

Ala Ala Ser Pro Tyr Leu Gly Leu His His Asp His His His His His
20          25          30

Gly Gly Gly Gly Gly Gly Gly Gly Met Asn Gly Arg His Met Ser Pro
35          40          45

```

MBI0058CIP.ST25.txt

Pro Thr Pro Pro Ala Ala Ala Glu Glu Ser Lys Ala Val Val Val Val
50 55 60

Ser Ser Ser Ala Thr Ala Ala Ala Arg Tyr Arg Glu Cys Leu Lys Asn
65 70 75 80

His Ala Ala Ala Ile Gly Gly Ser Ala Thr Asp Gly Cys Gly Glu Phe
85 90 95

Met Pro Gly Gly Glu Glu Gly Ser Leu Asp Ala Leu Arg Cys Ser Ala
100 105 110

Cys Gly Cys His Arg Asn Phe His Arg Lys Glu Leu Asp Ala Ala Ala
115 120 125

Ala Pro Pro Leu His His His His His Gln Leu Leu Gly Val Gly Ala
130 135 140

His Pro Arg Gly His Gly His His His His His Leu Leu Val Ala Ala
145 150 155 160

Leu Pro Pro Pro Thr Arg Met Val Met Pro Leu Ser Ala Met His Thr
165 170 175

Ser Glu Ser Asp Asp Ala Ala Ala Arg Pro Gly Gly Gly Ala Ala Ala
180 185 190

Arg Lys Arg Phe Arg Thr Lys Phe Thr Ala Glu Gln Lys Ala Arg Met
195 200 205

Leu Gly Phe Ala Glu Glu Val Gly Trp Arg Leu Gln Lys Leu Glu Asp
210 215 220

Ala Val Val Gln Arg Phe Cys Gln Glu Val Gly Val Lys Arg Arg Val
225 230 235 240

Leu Lys Val Trp Met His Asn Asn Lys His Thr Leu Ala Arg Arg His
245 250 255

Leu His Pro Ser Pro Ala Ala Ala Ala Gly Asp Asp Asp Asp Asp Gly
260 265 270

Ala Pro Pro Pro His Pro Asp Pro Arg Arg Arg Glu Leu Ala Ala Ala
275 280 285

Ala Ala Pro Pro Pro Ala Pro Val Thr Gln His Ile Lys Lys Ser Val
290 295 300

MBI0058CIP.ST25.txt

Asp Asn Lys Ser Leu Ile Ser Ser Leu Ala Ala Leu His Cys Ile Ala
305 310 315 320

Leu Leu Leu Phe His Gln Ile Asp Ala
325

<210> 117
<211> 1096
<212> DNA
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3685 Predicted polypeptide sequence is orthologous to G2999

<400> 117
taacccaaag ccatccagca ctttgcgagg tcgctttcgt ttcgcctcct tcgtcggccc 60
cggaccggac cggacagagg catgtcctga tggattcag gggccatgac gaaccgcgtc 120
acgagatggg agtcgcgtac ggcaggacgc caccctcctc ctctcctcc cccgccgcct 180
ccgcctccgc ggggaacggc gccggcgcgg cggaggtgag gtaccacgag tgcctgcgca 240
accacgccgc ggcgatgggc ggccacgtcg tggacggatg cagggagtgc atgccgatgc 300
cggggggacgc cgccgacgcc ctcaagtgcg ccgcctgcgg ctgccaccgc agcttcacc 360
gcaaggacga cgggcagcag cagcagcagc tgcgcctgct catcccgtcc ccgcccacgc 420
cgcgcgctccc gctgctcatg ccgccgccgc agccgcagcc gcacccgcac ccgcaacacc 480
cctacctgca cccgccgttc ccgtaccacc acaccccaag cggcagcggc ggcacgacga 540
ccgagtcgtc cagcgaggag cgggggcctc cctcctcgtc ggcggcggcg gcgcaggggc 600
ggcggaagcg gttccggacc aagttcacgc cggagcagaa ggagcagatg ctggcggttcg 660
cggagcgggt ggggtggcgg atgcagaagc aggacgaggc actcgtcgaa cagttctgcg 720
cgcaggtcgg cgtgcggcgc caggtgttca aggtgtggat gcacaacaac aagagcagca 780
tcggcagcag cagcggcggc ggcagtagga ggcagccgca ggagcaacag tcacaacagc 840
agcagcagca gcagtagcca tgggaggaga caagcatttg gttaatggtt tggtaaattcc 900
ccacctcatt atttttatac gcccaagaca tgaggagacg ggttaaacaa cgcaacggaa 960
gtgaggacta ctctctctgc gatctttatc ctctctctct ctctctctct ctcttcattt 1020
ggccttaacc ttcattcttt gtagtcactt atcctcctcc ataatttggt tcttgattct 1080
agccttgtcc aatttg 1096

<210> 118
<211> 255
<212> PRT
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3685 polypeptide Orthologous to G2999

<400> 118

Met Glu Phe Arg Gly His Asp Glu Pro Val Asp Glu Met Gly Val Ala
 1 5 10 15

Tyr Gly Arg Thr Pro Pro Ser Ser Ser Ser Ser Pro Ala Ala Ser Ala
 20 25 30

Ser Ala Gly Asn Gly Ala Gly Ala Ala Glu Val Arg Tyr His Glu Cys
 35 40 45

Leu Arg Asn His Ala Ala Ala Met Gly Gly His Val Val Asp Gly Cys
 50 55 60

Arg Glu Phe Met Pro Met Pro Gly Asp Ala Ala Asp Ala Leu Lys Cys
 65 70 75 80

Ala Ala Cys Gly Cys His Arg Ser Phe His Arg Lys Asp Asp Gly Gln
 85 90 95

Gln Gln Gln Gln Leu Arg Leu Leu Ile Pro Ser Pro Pro Thr Pro Arg
 100 105 110

Val Pro Leu Leu Met Pro Pro Pro Gln Pro Gln Pro His Pro His Pro
 115 120 125

Gln His Pro Tyr Leu His Pro Pro Phe Pro Tyr His His Thr Pro Ser
 130 135 140

Gly Ser Gly Gly Thr Thr Thr Glu Ser Ser Ser Glu Glu Arg Gly Pro
 145 150 155 160

Pro Ser Ser Ser Ala Ala Ala Ala Gln Gly Arg Arg Lys Arg Phe Arg
 165 170 175

Thr Lys Phe Thr Pro Glu Gln Lys Glu Gln Met Leu Ala Phe Ala Glu
 180 185 190

Arg Val Gly Trp Arg Met Gln Lys Gln Asp Glu Ala Leu Val Glu Gln
 195 200 205

Phe Cys Ala Gln Val Gly Val Arg Arg Gln Val Phe Lys Val Trp Met
 210 215 220

His Asn Asn Lys Ser Ser Ile Gly Ser Ser Ser Gly Gly Gly Ser Arg
 225 230 235 240

Arg Gln Pro Gln Glu Gln Gln Ser Gln Gln Gln Gln Gln Gln Gln
 245 250 255

<210> 119
 <211> 699
 <212> DNA
 <213> Oryza sativa (indica cultivar-group)

<220>
 <223> G3686 Predicted polypeptide sequence is orthologous to G2999

<400> 119
 atggagctca gcgagcacga ggaggacgcc ggcgacgtgg gcggtggctg ctcacccccg 60
 cccacgccgc ctcaccgcgt gctgacgtcg gccgcccccg agacgatcag gtgccggtac 120
 cacgagtgcc tccggaacca cgcgggcgcc tcggggcgcc acgtcgtgga tggctgcggc 180
 gagttcatgc cggcgtccac cgaggagccg ctgcctgctg cggcctgcgg ctgccaccgc 240
 agcttccacc gccgggaccc ttccccgggc cgcgcggggc cagcacggct gctgcagctg 300
 cacctgccgg cgtccatcaa ctgcgcgcga ccaccgcgc tgctgctgcc gcctgcagcg 360
 gccgccagca agcaaggttt gccgttcctt ggctacggca cgcccagcgg cggcactggc 420
 accacgaccg cgtcctccag cgacgagcgg ctgcggccct cgccggtgca gccacggagg 480
 cggtcacgca cgacgttcac gcgggagcag aaggagcaga tgctggcggt cgcgagcgc 540
 gtgggggtgga ggatccagcg gcaggaggag gcgacggtgg agcacttctg cgcgcaggtc 600
 ggcgtccgga ggcaagcgt caaggtgtgg atgcacaaca acaagcatag cttcaagcag 660
 aaacagcagc aggagaacag gcaggaacag cagcagtag 699

<210> 120
 <211> 232
 <212> PRT
 <213> Oryza sativa (indica cultivar-group)

<220>
 <223> G3686 polypeptide Orthologous to G2999

<400> 120

Met Glu Leu Ser Glu His Glu Glu Asp Ala Gly Asp Val Gly Gly Gly
 1 5 10 15

Cys Ser Ser Pro Pro Thr Pro Pro His Arg Val Leu Thr Ser Ala Ala
 20 25 30

Pro Glu Thr Ile Arg Cys Arg Tyr His Glu Cys Leu Arg Asn His Ala
 35 40 45

Ala Ala Ser Gly Gly His Val Val Asp Gly Cys Gly Glu Phe Met Pro
 50 55 60

Ala Ser Thr Glu Glu Pro Leu Ala Cys Ala Ala Cys Gly Cys His Arg
 65 70 75 80

Ser Phe His Arg Arg Asp Pro Ser Pro Gly Arg Ala Gly Ala Ala Arg
85 90 95

Leu Leu Gln Leu His Leu Pro Ala Ser Ile Asn Ser Arg Ala Pro Pro
100 105 110

Ala Leu Leu Leu Pro Pro Ala Ala Ala Ser Lys Gln Gly Leu Pro
115 120 125

Phe Pro Gly Tyr Gly Thr Pro Ser Gly Gly Thr Gly Thr Thr Thr Ala
130 135 140

Ser Ser Ser Asp Glu Arg Leu Arg Pro Ser Pro Val Gln Pro Arg Arg
145 150 155 160

Arg Ser Arg Thr Thr Phe Thr Arg Glu Gln Lys Glu Gln Met Leu Ala
165 170 175

Phe Ala Glu Arg Val Gly Trp Arg Ile Gln Arg Gln Glu Glu Ala Thr
180 185 190

Val Glu His Phe Cys Ala Gln Val Gly Val Arg Arg Gln Ala Leu Lys
195 200 205

Val Trp Met His Asn Asn Lys His Ser Phe Lys Gln Lys Gln Gln Gln
210 215 220

Glu Asn Arg Gln Glu Gln Gln Gln
225 230

<210> 121

<211> 1284

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3690 Predicted polypeptide sequence is orthologous to G2999

<400> 121

atggagtaca agagatcatc gcatgtggag gaggaggaag aggaggaaga agaggaggac 60

gacgaggagg aagacgagga ggagcaaggt caccatcagt acacgacggc ggcggcgag 120

cagcagctgc acccgaggt tcttggtctg tcggcttcct cgccgtcgtc gttgatggac 180

tccgccgctt tctcgaggcc cctcctgcct cccaacctgt cgctcgtgtc gccgtcggcg 240

gcggcgggcg cggcgcccg tggatcctac ctgcatgcgg ctcaccacca tgggcaggga 300

agaaggggtg aggcgcctgg tggggagagc cagcaccatc tccagcgcca tcatgagccg 360

gcgagaaatg gcgttcttgg cggcgtcgcc ggtgctcacg cggcgtctac gcttgccctc 420

MBI0058CIP.ST25.txt

```

gtgggtggtg gtgggtggtg tccgagaggg ggcgaggggg cggcgggcga ggcgccgacg 480
tggaggtaca gggagtgcct caagaaccac gcggcgcgga tgggcgcgca cgtgctcgac 540
ggctgcggcg agttcatgtc gtcccttggc gacggcgccg cggcgctggc ctgcccgcgcg 600
tgcggctgcc accgtagctt ccaccgccgc gagccggcgg tegtgcgcgc gccctcgctc 660
tcgctctgcc ccgcctccgc ctccgcctcc gccgcgcgcg gcctggtgtc cctatcccc 720
tccgcgacgc ccaccggcgc caactcctcc cggctcatgc cgtcctcct cgccccgcgcg 780
cacatgcaga agcgcgccgc cgtcctcccc gtgtccccgg cgtctgcgcc cgccgcgctg 840
gccgagtcgt caagcgagga gctgcgcccc ccgcgcgtcc cctcttccca cccccacgcg 900
cacgcggccg ccgtggtggc ggcgtcggcc tccgcgccgc cggggccgag caagaagcgc 960
ttccggacca agttcacggc ggagcagaag gagcggatgc gtgaattcgc gcaccgcgtc 1020
gggtggcgca tccacaagcc cgacgccgcc gccgtcgacg cgttctgcgc ccaggtcggc 1080
gtctcccgcc gcgtcctcaa ggtgtggatg cacaacaaca aacacctcgc caagacgccc 1140
ccgtcgcgga catcgcagcc gccgcgcgcg ccgtccacc acgatccttc tcctcctccc 1200
cctcctcacc accaccacca ccaccatcac caccaccacc caccacaaca ccatcagcag 1260
cagcagcagc agcatgatgc atga 1284

```

```

<210> 122
<211> 427
<212> PRT
<213> Oryza sativa (japonica cultivar-group)

```

```

<220>
<223> G3690 polypeptide Orthologous to G2999

```

<400> 122

```

Met Glu Tyr Lys Arg Ser Ser His Val Glu Glu Glu Glu Glu Glu Glu
1          5          10          15

```

```

Glu Glu Glu Asp Asp Glu Glu Glu Asp Glu Glu Glu Gln Gly His His
20          25          30

```

```

Gln Tyr Thr Thr Ala Ala Ala Gln Gln Gln Leu His Pro Gln Val Leu
35          40          45

```

```

Gly Ser Ser Ala Ser Ser Pro Ser Ser Leu Met Asp Ser Ala Ala Phe
50          55          60

```

```

Ser Arg Pro Leu Leu Pro Pro Asn Leu Ser Leu Val Ser Pro Ser Ala
65          70          75          80

```

```

Ala Ala Ala Ala Ala Pro Gly Gly Ser Tyr Leu His Ala Ala His His
85          90          95

```


His Gly Gln Gly Arg Arg Val Glu Ala Pro Gly Gly Glu Ser Gln His
100 105 110

His Leu Gln Arg His His Glu Pro Ala Arg Asn Gly Val Leu Gly Gly
115 120 125

Val Ala Gly Ala His Ala Ala Ser Thr Leu Ala Leu Val Gly Gly Gly
130 135 140

Gly Gly Gly Pro Arg Gly Gly Glu Gly Ala Ala Gly Glu Ala Pro Thr
145 150 155 160

Trp Arg Tyr Arg Glu Cys Leu Lys Asn His Ala Ala Arg Met Gly Ala
165 170 175

His Val Leu Asp Gly Cys Gly Glu Phe Met Ser Ser Pro Gly Asp Gly
180 185 190

Ala Ala Ala Leu Ala Cys Ala Ala Cys Gly Cys His Arg Ser Phe His
195 200 205

Arg Arg Glu Pro Ala Val Val Ala Pro Ala Ser Leu Ser Leu Cys Pro
210 215 220

Ala Ser Ala Ser Ala Ser Ala Ala Ala Gly Leu Val Ser Leu Ser Pro
225 230 235 240

Ser Ala Thr Pro Thr Gly Ala Asn Ser Ser Arg Leu Met Pro Leu Leu
245 250 255

Leu Ala Pro Pro His Met Gln Lys Arg Pro Pro Val Leu Pro Val Ser
260 265 270

Pro Ala Ser Ala Pro Ala Ala Leu Ala Glu Ser Ser Ser Glu Glu Leu
275 280 285

Arg Pro Pro Pro Leu Pro Ser Ser His Pro His Ala His Ala Ala Ala
290 295 300

Val Val Ala Ala Ser Ala Ser Ala Pro Pro Gly Pro Ser Lys Lys Arg
305 310 315 320

Phe Arg Thr Lys Phe Thr Ala Glu Gln Lys Glu Arg Met Arg Glu Phe
325 330 335

Ala His Arg Val Gly Trp Arg Ile His Lys Pro Asp Ala Ala Ala Val
340 345 350

MBI0058CIP.ST25.txt

Asp Ala Phe Cys Ala Gln Val Gly Val Ser Arg Arg Val Leu Lys Val
355 360 365

Trp Met His Asn Asn Lys His Leu Ala Lys Thr Pro Pro Ser Pro Thr
370 375 380

Ser Gln Pro Pro Pro Pro Pro Leu His His Asp Pro Ser Pro Pro Pro
385 390 395 400

Pro Pro His His His His His His His His His His His His Pro Pro Gln
405 410 415

His His Gln Gln Gln Gln Gln Gln His Asp Ala
420 425

<210> 123
<211> 717
<212> DNA
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3692 Predicted polypeptide sequence is orthologous to G2999

<400> 123
atggagcagc agcaggagcg gccgcgggag gtgtacaggg agtgcacgcg caaccacgcg 60
gcgaagctgg ggacctacgc gaacgacggc tgctgcgagt acacccccga cgacggccac 120
ccggcggggc tgctctgcgc ggcgtgcggc tgccaccgca acttccaccg gaaggacttc 180
ctcgacggcc gcgccaccgc cgcgcgggga ggggcgggag gcgccggcgt cggcgctcgcg 240
ccaatgctgc cggcccccg tggaggcggg ccgccgggat acatgcacat ggcggcgatg 300
ggaggagcgg tgggcggcgg cggcggcgctc gacggcgggc gcggctccgg ggggaggcgg 360
cggacgcgga ccaagtacac ggaggagcag aaggcgcgga tgctgcggtt cgcggagcgg 420
ctcgggtggc ggatgccgaa gcgggagccc ggcgcgcgc ccggggacga cgaggtggcg 480
cgcttctgcc gggagatcgg cgtcaaccgg caggtcttca aggtgtggat gcacaaccac 540
aaggccggcg gcggcgggcg cggcgggcggc agcgcgggcc ccggcgccgg tggaggcgcc 600
cagacgtcgt cgtcgacgac caggggcggc ggcgacgtcg ggggtgggctt gtcgccggcg 660
atgggcggcg acggcgagga cgacgaggag gtgaggggga gcgagatgtg catgtag 717

<210> 124
<211> 238
<212> PRT
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3692 polypeptide Orthologous to G2999

<400> 124

Met Glu Gln Gln Gln Glu Arg Pro Arg Glu Val Tyr Arg Glu Cys Met
 1 5 10 15

Arg Asn His Ala Ala Lys Leu Gly Thr Tyr Ala Asn Asp Gly Cys Cys
 20 25 30

Glu Tyr Thr Pro Asp Asp Gly His Pro Ala Gly Leu Leu Cys Ala Ala
 35 40 45

Cys Gly Cys His Arg Asn Phe His Arg Lys Asp Phe Leu Asp Gly Arg
 50 55 60

Ala Thr Ala Ala Ala Gly Gly Ala Gly Gly Ala Gly Val Gly Val Ala
 65 70 75 80

Pro Met Leu Pro Ala Pro Gly Gly Gly Gly Pro Pro Gly Tyr Met His
 85 90 95

Met Ala Ala Met Gly Gly Ala Val Gly Gly Gly Gly Gly Val Asp Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Arg Arg Arg Thr Arg Thr Lys Phe Thr Glu
 115 120 125

Glu Gln Lys Ala Arg Met Leu Arg Phe Ala Glu Arg Leu Gly Trp Arg
 130 135 140

Met Pro Lys Arg Glu Pro Gly Arg Ala Pro Gly Asp Asp Glu Val Ala
 145 150 155 160

Arg Phe Cys Arg Glu Ile Gly Val Asn Arg Gln Val Phe Lys Val Trp
 165 170 175

Met His Asn His Lys Ala Gly Gly Gly Gly Gly Gly Gly Gly Ser Gly
 180 185 190

Gly Pro Gly Ala Gly Gly Gly Ala Gln Thr Ser Ser Ser Thr Thr Arg
 195 200 205

Gly Gly Gly Asp Val Gly Val Gly Leu Ser Pro Ala Met Gly Gly Asp
 210 215 220

Gly Glu Asp Asp Glu Glu Val Arg Gly Ser Glu Met Cys Met
 225 230 235

<210> 125

<211> 765

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3694 Predicted polypeptide sequence is orthologous to G2999

<400> 125

```

atgggcgcg c acgtgctcga cggctgcggc gagttcatgt cgtcccctgg cgacggcgcc      60
gcggcgctgg cctgcgcgcg gtgcggctgc caccgtagct tccaccgccg cgagccggcg      120
gtcgtcgcgc cggcctcgct ctgcgtctgc cccgcctccg cctccgcctc cgccgcgcgc      180
ggcctggtgt ccctatcccc ctccgcgacg cccaccggcg ccaactcctc ccggctcatg      240
ccgctcctcc tcgccccgcc gcacatgcag aagcgcccg ccgctcctcc cgtgtccccg      300
gcgtctgcgc ccgccgcgct ggccgagtcg tcaagcgagg agctgcgccc gccgccgctc      360
ccctcttccc acccccacgc gcacgcggcc gccgtggtgg cggcgtcggc ctccgcgcgc      420
ccggggccga gcaagaagcg cttccggacc aagttcacgg cggagcagaa ggagcggatg      480
cgtgaattcg cgcaccgcgt cgggtggcgc atccacaagc ccgacgccgc cgccgtcgac      540
gcgttctgcg cccaggtcgg cgtctccgcg cgcgtcctca aggtgtggat gcacaacaac      600
aaactcctcg ccaagacgcc cccgtcgcag acatggcagc cgccgccgcc gccgctccac      660
cacgatcctt ctctcctcc cctcctcac caccaccacc accaccatca ccaccaccac      720
ccaccacaac accatcagca gcagcagcag cagcatgatg catga                      765

```

<210> 126

<211> 254

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3694 polypeptide Orthologous to G2999

<400> 126

```

Met Gly Ala His Val Leu Asp Gly Cys Gly Glu Phe Met Ser Ser Pro
1              5              10              15

Gly Asp Gly Ala Ala Ala Leu Ala Cys Ala Ala Cys Gly Cys His Arg
                20              25              30

Ser Phe His Arg Arg Glu Pro Ala Val Val Ala Pro Ala Ser Leu Ser
          35              40              45

Leu Cys Pro Ala Ser Ala Ser Ala Ser Ala Ala Ala Gly Leu Val Ser
          50              55              60

Leu Ser Pro Ser Ala Thr Pro Thr Gly Ala Asn Ser Ser Arg Leu Met
65              70              75              80

```

MBI0058CIP.ST25.txt

Pro Leu Leu Leu Ala Pro Pro His Met Gln Lys Arg Pro Pro Val Leu
85 90 95

Pro Val Ser Pro Ala Ser Ala Pro Ala Ala Leu Ala Glu Ser Ser Ser
100 105 110

Glu Glu Leu Arg Pro Pro Pro Leu Pro Ser Ser His Pro His Ala His
115 120 125

Ala Ala Ala Val Val Ala Ala Ser Ala Ser Ala Pro Pro Gly Pro Ser
130 135 140

Lys Lys Arg Phe Arg Thr Lys Phe Thr Ala Glu Gln Lys Glu Arg Met
145 150 155 160

Arg Glu Phe Ala His Arg Val Gly Trp Arg Ile His Lys Pro Asp Ala
165 170 175

Ala Ala Val Asp Ala Phe Cys Ala Gln Val Gly Val Ser Arg Arg Val
180 185 190

Leu Lys Val Trp Met His Asn Asn Lys Leu Leu Ala Lys Thr Pro Pro
195 200 205

Ser Gln Thr Trp Gln Pro Pro Pro Pro Pro Leu His His Asp Pro Ser
210 215 220

Pro Pro Pro Pro Pro His His His His His His His His His His His
225 230 235 240

Pro Pro Gln His His Gln Gln Gln Gln Gln Gln His Asp Ala
245 250

<210> 127

<211> 855

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3695 Predicted polypeptide sequence is orthologous to G2999

<400> 127

atgatggatc acctgagcct ggtgccctac gagggcgcca gcgccggcgg gggaggaggt 60

ggaggggaagt acaaggagt catgcggaac cacgcggcgg cgatgggcgg gcaggcgttc 120

gacgggtgcg gggagtacat gccggcgctc cccgactcgc tcaagtgcgc cgcgtgcggc 180

tgccaccgca gcttcaccg ccgcgccgcc gcgggcatcg gcggcgggcc ggtgttcttc 240

cgccccccgc caccgccga gccgcactcg caccacgccg cgctgcaggg cttcctcccc 300

tcgtccgtgc cggcgccggc gccgccgccg cagctcgcgc tgccgtacca cgccgtgccc 360

MBI0058CIP.ST25.txt

```

gccgcggcgt ggcaccacgc ggcggcgccg gcggcaggcc gcgccggctc ggagacgccc 420
ccgcgggatgg acgacttcgg ccccggcagc gccggcgcca gcgggagcgg cggcgccggc 480
atcttcgggc ggaagcgggt ccggaccaag ttcacgccgg agcagaagga gcggatgcgg 540
gagttcgccg agaagcaagg gtggcgcatc aaccgcaacg acgacggcgc cctggaccgc 600
ttctgcgtcg agatcggcgt caagcgccac gtctcaagg tctggatgca caaccacaag 660
aaccagctcg cctcctcccc gacctccgcc gccgccgccg ccgccggcgt catgaacccc 720
ggcgccggca tcggcctcgg caccggcctc ggcaccggca tcagcggcga cggcgacggc 780
gacgacgacg acaccgacga ctccccgccc cgcgcgcgcc tgctctcccc ctccccttca 840
ccgatcagcg tctag 855

```

```

<210> 128
<211> 284
<212> PRT
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3695 polypeptide Orthologous to G2999.

<400> 128

```

```

Met Met Asp His Leu Ser Leu Val Pro Tyr Glu Gly Gly Ser Ala Gly
1          5          10          15

Gly Gly Gly Gly Gly Gly Lys Tyr Lys Glu Cys Met Arg Asn His Ala
20          25          30

Ala Ala Met Gly Gly Gln Ala Phe Asp Gly Cys Gly Glu Tyr Met Pro
35          40          45

Ala Ser Pro Asp Ser Leu Lys Cys Ala Ala Cys Gly Cys His Arg Ser
50          55          60

Phe His Arg Arg Ala Ala Ala Gly Ile Gly Gly Gly Pro Val Phe Phe
65          70          75          80

Arg Pro Pro Pro Pro Pro Gln Pro His Ser His His Ala Ala Leu Gln
85          90          95

Gly Phe Leu Pro Ser Ser Val Pro Ala Pro Ala Pro Pro Pro Gln Leu
100         105         110

Ala Leu Pro Tyr His Ala Val Pro Ala Ala Ala Trp His His Ala Ala
115         120         125

Ala Ala Ala Ala Gly Arg Ala Gly Ser Glu Thr Pro Pro Arg Met Asp
130         135         140

```

MBI0058CIP.ST25.txt

Asp Phe Gly Pro Gly Ser Ala Gly Gly Ser Gly Ser Gly Gly Gly Gly
145 150 155 160

Ile Phe Gly Arg Lys Arg Phe Arg Thr Lys Phe Thr Pro Glu Gln Lys
165 170 175

Glu Arg Met Arg Glu Phe Ala Glu Lys Gln Gly Trp Arg Ile Asn Arg
180 185 190

Asn Asp Asp Gly Ala Leu Asp Arg Phe Cys Val Glu Ile Gly Val Lys
195 200 205

Arg His Val Leu Lys Val Trp Met His Asn His Lys Asn Gln Leu Ala
210 215 220

Ser Ser Pro Thr Ser Ala Ala Ala Ala Ala Ala Gly Val Met Asn Pro
225 230 235 240

Gly Ala Gly Ile Gly Leu Gly Thr Gly Leu Gly Thr Gly Ile Ser Gly
245 250 255

Asp Gly Asp Gly Asp Asp Asp Asp Thr Asp Asp Ser Pro Pro Arg Ala
260 265 270

Ala Val Ser Ser Pro Ser Pro Ser Pro Ile Ser Val
275 280

<210> 129
<211> 999
<212> DNA
<213> Zea mays

<220>
<223> G3719 Predicted polypeptide sequence is orthologous to G1274

<400> 129
ctgccggcgc gtgcgtctac ttactcaggc ggctctgcta ggactcgccc acgagacgag 60
ctacgccgcc tactaccgc cgccgcgcc cgcctcctcg tacttcccac caccaccga 120
cctcgtggcg gacctccgc cgccgcgc cgccaccatg gccgatgact acttccagtt 180
cgggttcacc ggccaggaga tgggtggcga tgactgctcg gcgccggtgt tcgccaacag 240
ttcttcagac gccgtcaccg ccgccgtcgg caatggcatg agcctgctga gctacggcgt 300
ggacggcgac ggcgacggga ggaggccgat gagcggacca ccatatggca ccggtgggaa 360
cggcggcggc cggccgccgt cgtcgtcacg gatcgggttc cggacgcggt cggaggtgga 420
cgtgctggac gatggcttca agtggcgcaa gtacggcaag aaggcgggtca agagcagccc 480
caacccgagg aactactacc ggtgctcgac ggagggctcc ggcgtgaaga agcgcgtgga 540

```

gcgggacagc gacgaccgc gctacgtcgt caccacctac gacggcgtcc acaaccacgc      600
cgcgccggggc ccgggcgcgc cctcctacct gtgccaaacca ccgccgccgc gcggcgcaac      660
cgcgaccgca acgcccttct cgcctccacg ctcggcctcg gcgccagcgc ctctggctgc      720
agcgcccagc tggagcgccg cctgtgacgc gtggtgggag gcgcagctgc acgccgcggc      780
ggcggttgct cattcctcgg agtcgtcgta ctgatccgat ccgtcatcca tcagttatta      840
cacgcacgta cgggtcacgt agctagaatg tgttggaact ctaaaacgct cacaagcaca      900
ggacacagat tggtgagagg aggaagacga atgaacagta gctaaacca aagagttggg      960
cgcccaaaca cctgcagcgc tccgaccctg cttttctct      999

```

```

<210> 130
<211> 218
<212> PRT
<213> Zea mays

```

```

<220>
<223> G3719 polypeptide Orthologous to G1274
<400> 130

```

```

Met Ala Asp Asp Tyr Phe Gln Phe Gly Phe Thr Gly Gln Glu Met Val
1           5           10          15

```

```

Ala Asp Asp Cys Ser Ala Pro Val Phe Ala Asn Ser Ser Ser Asp Ala
          20          25          30

```

```

Val Thr Ala Ala Val Gly Asn Gly Met Ser Leu Leu Ser Tyr Gly Val
          35          40          45

```

```

Asp Gly Asp Gly Asp Gly Arg Arg Pro Met Ser Gly Pro Pro Tyr Gly
          50          55          60

```

```

Thr Gly Gly Asn Gly Gly Gly Arg Pro Pro Ser Ser Ser Arg Ile Gly
          65          70          75          80

```

```

Phe Arg Thr Arg Ser Glu Val Asp Val Leu Asp Asp Gly Phe Lys Trp
          85          90          95

```

```

Arg Lys Tyr Gly Lys Lys Ala Val Lys Ser Ser Pro Asn Pro Arg Asn
          100          105          110

```

```

Tyr Tyr Arg Cys Ser Thr Glu Gly Ser Gly Val Lys Lys Arg Val Glu
          115          120          125

```

```

Arg Asp Ser Asp Asp Pro Arg Tyr Val Val Thr Thr Tyr Asp Gly Val
          130          135          140

```


MBI0058CIP.ST25.txt

His Asn His Ala Ala Pro Gly Pro Gly Ala Ala Ser Tyr Leu Cys Gln
145 150 155 160

Pro Pro Pro Pro Arg Gly Ala Thr Ala Thr Ala Thr Pro Phe Ser Pro
165 170 175

Pro Arg Ser Ala Ser Ala Pro Ala Pro Leu Ala Ala Ala Pro Ser Trp
180 185 190

Ser Ala Ala Cys Asp Ala Trp Trp Glu Ala Gln Leu His Ala Ala Ala
195 200 205

Ala Val Ala His Ser Ser Glu Ser Ser Tyr
210 215

<210> 131
<211> 666
<212> DNA
<213> Zea mays

<220>
<223> G3720 Predicted polypeptide sequence is orthologous to G1274

<400> 131
atggcggcag tcggagctca cccagtgtctg taccaccacc cggcgccggc gggcgacgcc 60
tcttccatgt cctcctactt ctccacgga ggcagctcca ccacctccag ctctgcgtcc 120
agcttcaccg ccgcgctcgc gccgacgacg acggcgctcg ccgagcattt cgacatctcc 180
gagttcctct tcgacgacgc tgcgggcgct ggggtcgccg gcgcgccagg tgtgttcgcc 240
gatggcgccg cccgccccgt cgtcctgccc gtgcgggatg ccgctggtgg tgggtgcaatt 300
atcggcgccg ccgctggggg cgcggtgctg gcgtcggagg tgccagagcg gccgcggacg 360
acgcggatcg cgttcgagac gaggtcggag atcgagatcc tggacgacgg ctacaagtgg 420
aggaagtacg gcaagaagtc cgtcaagaac agccccaacc caaggaacta ctaccggtgc 480
tcgacggaag ggtgcaacgt gaagaagcgg gtggagcggg acaaggacga cccagctac 540
gtggtgacga cgtacgaggg gatgcacaac cacgtcagcc ccagtacggt gtactacgcc 600
agccaggacg ccgcctccgg ccgcttcttc gtcgccggca cgcagccacc gggctccctc 660
aactga 666

<210> 132
<211> 221
<212> PRT
<213> Zea mays

<220>
<223> G3720 polypeptide Orthologous to G1274

<400> 132

MBI0058CIP.ST25.txt

Met Ala Ala Val Gly Ala His Pro Val Leu Tyr His His Pro Ala Pro
1 5 10 15

Ala Gly Asp Ala Ser Ser Met Ser Ser Tyr Phe Ser His Gly Gly Ser
20 25 30

Ser Thr Thr Ser Ser Ser Ala Ser Ser Phe Thr Ala Ala Leu Ala Pro
35 40 45

Thr Thr Thr Ala Leu Ala Glu His Phe Asp Ile Ser Glu Phe Leu Phe
50 55 60

Asp Asp Ala Ala Gly Ala Gly Val Ala Gly Ala Pro Gly Val Phe Ala
65 70 75 80

Asp Gly Ala Ala Arg Pro Val Val Leu Pro Val Pro Asp Ala Ala Gly
85 90 95

Gly Gly Ala Ile Ile Gly Ala Ala Ala Gly Gly Ala Ala Ala Ala Ser
100 105 110

Glu Val Pro Glu Arg Pro Arg Thr Thr Arg Ile Ala Phe Arg Thr Arg
115 120 125

Ser Glu Ile Glu Ile Leu Asp Asp Gly Tyr Lys Trp Arg Lys Tyr Gly
130 135 140

Lys Lys Ser Val Lys Asn Ser Pro Asn Pro Arg Asn Tyr Tyr Arg Cys
145 150 155 160

Ser Thr Glu Gly Cys Asn Val Lys Lys Arg Val Glu Arg Asp Lys Asp
165 170 175

Asp Pro Ser Tyr Val Val Thr Thr Tyr Glu Gly Met His Asn His Val
180 185 190

Ser Pro Ser Thr Val Tyr Tyr Ala Ser Gln Asp Ala Ala Ser Gly Arg
195 200 205

Phe Phe Val Ala Gly Thr Gln Pro Pro Gly Ser Leu Asn
210 215 220

<210> 133

<211> 825

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3721 Predicted polypeptide sequence is orthologous to G1274

MBI0058CIP.ST25.txt

```

<400> 133
agtggatccc ccgggctgga ggaaaattca ccggtgaaaa gggttcagcac tgtgcaatgg      60
cggcttccgt aggactgaac cctgaagctt tcttcttcag caactcctac tcctactcct      120
catccccttt catggccagc tacacgccgg agttctcggc cgccgctatc gacgccaact      180
tattctccgg cgagctcgat ttcgactgct ctctcccagc tccggcccag gagtaccgg      240
aaaatgaaaa cactatgatg aggtacgaga gcgaggagaa gatgagggcg aggggtgaacg      300
ggaggatcgg gttcaggacg aggtcggagg tggagattct tgatgatggc ttcaagtgga      360
ggaagtacgg caagaaagct gtcaagaaca gcccaaatcc aagaaactac taccggtgct      420
cgacggagggg gtgcaacgtg aagaagcgag tggagagaga ccgggaggac caccgctacg      480
tcataccac ctacgacggc gtccacaacc acgcgagccc cgccgccgcc gccgcggcgc      540
tgcagtacgc cgccgccgcc ggcgactact acagcccgcc gctcagcagc gccggctcgc      600
cgccggccgc ctatttcggc aggcggcttc gctgctcttc tgagggctga tgaagtttgt      660
ctaggactag acacgcccgg gagctctagc taggatagaa aactagagaa agtttaatta      720
tacctgaatt ttaattaatc acctcacaaa actctgatgt atcataattat atcgtgatag      780
tgactggttg ttaatttaat tttggcgatc gatgtgatct tcggt      825

```

```

<210> 134
<211> 197
<212> PRT
<213> Oryza sativa (japonica cultivar-group)

```

```

<220>
<223> G3721 polypeptide Orthologous to G1274

```

<400> 134

```

Met Ala Ala Ser Val Gly Leu Asn Pro Glu Ala Phe Phe Phe Ser Asn
1          5          10          15

```

```

Ser Tyr Ser Tyr Ser Ser Ser Pro Phe Met Ala Ser Tyr Thr Pro Glu
          20          25          30

```

```

Phe Ser Ala Ala Ala Ile Asp Ala Asn Leu Phe Ser Gly Glu Leu Asp
          35          40          45

```

```

Phe Asp Cys Ser Leu Pro Ala Pro Ala Gln Glu Tyr Pro Glu Asn Glu
          50          55          60

```

```

Asn Thr Met Met Arg Tyr Glu Ser Glu Glu Lys Met Arg Ala Arg Val
          65          70          75          80

```

```

Asn Gly Arg Ile Gly Phe Arg Thr Arg Ser Glu Val Glu Ile Leu Asp
          85          90          95

```

MBI0058CIP.ST25.txt

Asp Gly Phe Lys Trp Arg Lys Tyr Gly Lys Lys Ala Val Lys Asn Ser
100 105 110

Pro Asn Pro Arg Asn Tyr Tyr Arg Cys Ser Thr Glu Gly Cys Asn Val
115 120 125

Lys Lys Arg Val Glu Arg Asp Arg Glu Asp His Arg Tyr Val Ile Thr
130 135 140

Thr Tyr Asp Gly Val His Asn His Ala Ser Pro Ala Ala Ala Ala Ala
145 150 155 160

Ala Leu Gln Tyr Ala Ala Ala Ala Gly Asp Tyr Tyr Ser Pro Pro Leu
165 170 175

Ser Ser Ala Gly Ser Pro Pro Ala Ala Tyr Phe Gly Arg Arg Leu Arg
180 185 190

Cys Ser Ser Glu Gly
195

<210> 135

<211> 834

<212> DNA

<213> Zea mays

<220>

<223> G3722 Predicted polypeptide sequence is orthologous to G1274

<400> 135

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ccgtgcagcg gtgcttcag ctacttgggc tctcagcccc cgcccccttt cccgtcggca 180

gcgttcggcg cggtggcgca gctggacgtc ttgactgcc tgtcgtcgga cgaaggcggt 240

ggcgtccccg cagctgtacc tgggtgcgttc gcgccgcgc cgccgcttat gccggccgag 300

cgcgctcgtcc cggacgtgc tgcaggctac agtagtcata ctaggagtgc agcggctgtg 360

gcgggtgagg ggtcgaggac tacgcacaga attgcgttcc gagtgaggtc ggacgaggac 420

gagggtactcg acgacggcta caaatggagg aagtacggaa agaagtccgt caagaacagc 480

cctaataccga ggaactacta ccggtgctcg acggagggtc gcaacgtcaa gaaaagggtg 540

gagcgagaca gggacgaccc gagatacgtt gtgaccatgt acgagggagt gcacaacat 600

gtgagtcctg gtaccgtcta ttacgccacc cagcagccg cctccggccg cttcttcgtc 660

gccgggatgc atcagccagg ccattgatca acgagcagat cagagagcgt cttaattagt 720

gtaagatatg tataccgact atctgtttta ggccttggtc atgttttagg tcttgtccag 780

ttattccaaa tcatatagat tggaatgtat tgaaatgaat tgagatagat ttag 834

<210> 136
 <211> 213
 <212> PRT
 <213> Zea mays

<220>
 <223> G3722 polypeptide Orthologous to G1274

<400> 136

Met His Met Ala Leu Ser Ser Arg Ser Ser Phe Ala Ala Asp Val Leu
 1 5 10 15

Leu Pro Ala Thr Met Ser Tyr Arg Gln Pro Cys Ser Gly Ala Ser Ser
 20 25 30

Tyr Leu Gly Ser Gln Pro Ala Ala Pro Phe Pro Ser Ala Ala Phe Gly
 35 40 45

Ala Val Ala Gln Leu Asp Val Phe Asp Cys Leu Ser Ser Asp Glu Gly
 50 55 60

Val Gly Val Pro Ala Ala Val Pro Gly Ala Phe Ala Pro Pro Pro Pro
 65 70 75 80

Leu Met Pro Ala Glu Arg Val Val Pro Asp Ala Ala Ala Gly Tyr Ser
 85 90 95

Ser His Thr Arg Ser Ala Ala Ala Val Ala Gly Glu Gly Ser Arg Thr
 100 105 110

Thr His Arg Ile Ala Phe Arg Val Arg Ser Asp Glu Asp Glu Val Leu
 115 120 125

Asp Asp Gly Tyr Lys Trp Arg Lys Tyr Gly Lys Lys Ser Val Lys Asn
 130 135 140

Ser Pro Asn Pro Arg Asn Tyr Tyr Arg Cys Ser Thr Glu Gly Cys Asn
 145 150 155 160

Val Lys Lys Arg Val Glu Arg Asp Arg Asp Asp Pro Arg Tyr Val Val
 165 170 175

Thr Met Tyr Glu Gly Val His Asn His Val Ser Pro Gly Thr Val Tyr
 180 185 190

Tyr Ala Thr His Asp Ala Ala Ser Gly Arg Phe Phe Val Ala Gly Met
 195 200 205

His Gln Pro Gly His
210

<210> 137
<211> 1235
<212> DNA
<213> Glycine max

<220>
<223> G3723 Predicted polypeptide sequence is orthologous to G1274

<400> 137
gtcttgacgg tcccatthttc accccattgt gcaaattgaa agtagtaggg aaccctact 60
atagctacta catcatcaca atgacgtcac cttaacgtct ctcggtgtga cacgtagctc 120
agtgaggcta tttcgctgca tcctccaaga aggtgtttgg aaggatcctt cccaccccat 180
gccaaaagca agcatattaa ttaaaaaaaaa tagaaaaaaaa taaaacacaa ttttatttta 240
ttataggata tttattagtt atttattgga tataagtggc agcatgcttt agtcctaggc 300
gtgataaaag gccaaagact cttaggthttt tggctctttg cagaatcttt gagtgacaca 360
tacctagcta tcacctcaat ggattactat tttggaaacc ttaatcctaa cccttattac 420
catcactctg ccgtagtga catggcatct cctcctccg agttcatgtt atctgattat 480
ctcggtgttg aagatgctct tgttggtgat catcatcaag agtcttggtc acaaagcact 540
gaaactgaat catcggagaa agcaacctcc agcgatgcaa gtcattgggtt cgggtgatgca 600
acctccacca acaccaacat gcatataaag tgccaaaata gtgggattaa gggaaagaat 660
gcagaagtga gtcaaaggat cacgtthtaga accagatcgc aacttgaggt tatggatgat 720
ggatataaat ggaggaaata cggaagaaa acagtgaaga gcagtcccaa cccacggaac 780
tactacaagt gttcaggtga aggatgcgat gtgaagaaaa ggggtggaaag ggatagggat 840
gactcraact atgtgttaac aacgtacgac ggtgtccaca atcatcagac cccgtctact 900
gcctactaca gccaaatgcc cttgctgcat tctaatactg attggggcct ccacccttct 960
gcaaactcat aatatcctcc ttaatatagt aatatccaga gataggagaa tcaacttata 1020
cttttaggat tactttttat ctttattatt tttttttat aagagatttt aaaaaataaa 1080
taatgagaat agagaataat tttaaaagaa ttattgttga tgtaagttaa tctctactct 1140
gtatatatat atagttattg actcatttag tatattgcct gtcaataacc attattacat 1200
gtatattgat tattatgcag gttccctcc acgct 1235

<210> 138
<211> 197
<212> PRT
<213> Glycine max

<220>
<223> G3723 polypeptide Orthologous to G1274

<400> 138

Met Asp Tyr Tyr Phe Gly Asn Leu Asn Pro Asn Pro Tyr Tyr His His
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Ser Ala Val Val Asn Met Ala Ser Pro Ser Ser Glu Phe Met Leu Ser
20 25 30

Asp Tyr Leu Val Leu Glu Asp Ala Leu Val Val Asp His His Gln Glu
35 40 45

Ser Trp Ser Gln Ser Thr Glu Thr Glu Ser Ser Glu Lys Ala Thr Ser
50 55 60

Ser Asp Ala Ser His Gly Phe Gly Asp Ala Thr Ser Thr Asn Thr Asn
65 70 75 80

Met His Ile Lys Cys Gln Asn Ser Gly Ile Lys Gly Lys Asn Ala Glu
85 90 95

Val Ser Gln Arg Ile Thr Phe Arg Thr Arg Ser Gln Leu Glu Val Met
100 105 110

Asp Asp Gly Tyr Lys Trp Arg Lys Tyr Gly Lys Lys Thr Val Lys Ser
115 120 125

Ser Pro Asn Pro Arg Asn Tyr Tyr Lys Cys Ser Gly Glu Gly Cys Asp
130 135 140

Val Lys Lys Arg Val Glu Arg Asp Arg Asp Asp Ser Asn Tyr Val Leu
145 150 155 160

Thr Thr Tyr Asp Gly Val His Asn His Gln Thr Pro Ser Thr Ala Tyr
165 170 175

Tyr Ser Gln Met Pro Leu Leu His Ser Asn His Asp Trp Ala Leu His
180 185 190

Pro Ser Ala Asn Ser
195

<210> 139

<211> 974

<212> DNA

<213> Glycine max

<220>

<223> G3724 Predicted polypeptide sequence is orthologous to G1274

<400> 139

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60

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agttatcagc aatggacttc tacttttgaa actctctccc ttatcccaat aattatgctc 120
ataattctct taatatggct ctatcttccc ctgagattgc actatccgat tatctcatgc 180
tcgatgacta tgttgatcat caagattctc gatcatcaca aagcaccgag tcatctgaaa 240
aagcaacctt caatgatgcc actcacggat tcagtactgg tgcaacctct aagaataata 300
acataaactg caaaaatggg attaataaaa acaaagggtgg agtgggtcca aggatcgcggt 360
ttagaaccac atcagagctt gagatcatgg atgatggata caagtggagg aagtacggca 420
agaagtccgt gaagagcagt cccaatctaa ggaactacta caaatgttca agtggaggat 480
gcagtgtgaa gaaaagggtg gaaagggata gagatgacta cagctacgtg ataacaacat 540
atgaagggtg gcacaatcat gagagcccat ttaccacata ctacagcccc atctccttcg 600
tacattctga tactactttc aaatgacacc aacttcaaac ccttttgggc atttacacct 660
ccctagctta attatgtgcc aagaaaaagc ttggaagatt cgatcgagca ggggaagcta 720
tgtatcattg cattgtctaa tcaatcataa tttattttca tgctgtaata ggttgaagag 780
agtttctata cctttttttg gttccacgtt taatatatct ctcaattaaa aatcagcctt 840
tgctagtcca tgtaacaagg aacatgattc tccatgtgta aagttgttca aatcttaaaa 900
gtaagtatct tgtattagga ttagagtatc tctcttgtag tctgtttaat aataaaagtt 960
ttgcctccta aaaa 974

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<210> 140
 <211> 184
 <212> PRT
 <213> Glycine max

<220>
 <223> G3724 polypeptide Orthologous to G1274

<400> 140

Met Asp Phe Tyr Phe Gly Asn Ser Pro Pro Tyr Pro Asn Asn Tyr Ala
 1 5 10 15

His Asn Ser Leu Asn Met Ala Leu Ser Ser Pro Glu Ile Ala Leu Ser
 20 25 30

Asp Tyr Leu Met Leu Asp Asp Tyr Val Asp His Gln Asp Ser Arg Ser
 35 40 45

Ser Gln Ser Thr Glu Ser Ser Glu Lys Ala Thr Phe Asn Asp Ala Thr
 50 55 60

His Gly Phe Ser Thr Gly Ala Thr Ser Lys Asn Asn Asn Ile Asn Cys
 65 70 75 80

MBI0058CIP.ST25.txt

Lys Asn Gly Ile Asn Glu Asn Lys Gly Gly Val Gly Pro Arg Ile Ala
85 90 95

Phe Arg Thr Lys Ser Glu Leu Glu Ile Met Asp Asp Gly Tyr Lys Trp
100 105 110

Arg Lys Tyr Gly Lys Lys Ser Val Lys Ser Ser Pro Asn Leu Arg Asn
115 120 125

Tyr Tyr Lys Cys Ser Ser Gly Gly Cys Ser Val Lys Lys Arg Val Glu
130 135 140

Arg Asp Arg Asp Asp Tyr Ser Tyr Val Ile Thr Thr Tyr Glu Gly Val
145 150 155 160

His Asn His Glu Ser Pro Phe Thr Thr Tyr Tyr Ser Pro Ile Ser Phe
165 170 175

Val His Ser Asp Thr Thr Phe Lys
180

<210> 141
<211> 1369
<212> DNA
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3725 Predicted polypeptide sequence is orthologous to G1274

<400> 141
atgggcttcg ccaaaacaac aaccgaaacg gatatacaat tgtttcttat ggggccgtgc 60
ggggcatcaa agcaaaacaa ttcgaaacgg ggcggctcgc gcacggctcgc gcgcgccgaa 120
gcttcatcca acgactcgag ccaggaagct cgacggctct tgcggcgcgtg tcacgtaaga 180
gagtcygcc aaccacatgc acgtgtaccg atgtacatgg cggcggcggc tgcgggagca 240
agcacaccct tcaatttttg ccgccacggc tcgcacgccg agtacgacgc cgtcttcagc 300
ggcagctgga tggcgcgccg cccctccgcg gcgccgcacg gtggcggcgc ctccggctcc 360
ggctccggca gcggctacgg cgccgcctcg tacgttgctc ccaccttcgg cgcggcgttt 420
aggcagcagc atctcgacct cctcgactac ctgtccgacg atcagggcgt tccggcgcca 480
ccaccagcgg ctgtgcccag cgcgtcgtac gtgacgccgg cgccggcgat ggcccccgct 540
gaaccggctg tgccggatgc tgttgccgcc gccggcggct atccgaggag cgtggctgcg 600
gcggcgggcg ccgtggccgg cgaggggaaga gatcgacga cgacggacaa gatcgcattc 660
cggacgaggt cggacgatga gatactcgac gacgggtata agtggaggaa gtacgggaaa 720
aagtccgtta agaacagccc taatccgagg aactactacc ggtgctcgac ggaggggtgc 780
aacgtgaaga agaggggtgga gagagacaag aacgacccgc ggtacgtggt gacgatgtac 840

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gaggggatcc acaaccacgt gtgccccggc actgtctact acgccgcgca ggacgccgcc 900
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 tttgccggcc cagctgtggc ttagcttgat gtgcagctct agttattgta tgggctgtac 1020
 gggttcagtta tttgaagcgg gttataactta tatgttggtta atgtttgcct actgatttta 1080
 attaattttct tagagttaga ctcaatttgg cggaggggatt cccttcaaaa aaagaaatcc 1140
 cttcaaaaaa tttggcggag ggacgactga tatatatggt gacattagct aggtttgctc 1200
 acttttggca aaaataacaa gtttcctttc gtgccactct ccgtccctag gtcagtgttt 1260
 ggcaaaacgc ccaaaaaaat gtccgtgttg ccaattaatt tgcgattgt gtacttcaat 1320
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<210> 142
 <211> 243
 <212> PRT
 <213> Oryza sativa (japonica cultivar-group)

<220>
 <223> G3725 polypeptide Orthologous to G1274

<400> 142

Met Ala Ala Ala Ala Ala Gly Ala Ser Thr Pro Phe Asn Phe Cys Arg
 1 5 10 15

His Gly Ser His Ala Glu Tyr Asp Ala Val Phe Ser Gly Ser Trp Met
 20 25 30

Ala Arg Arg Pro Ser Ala Ala Pro His Gly Gly Gly Ala Ser Gly Ser
 35 40 45

Gly Ser Gly Ser Gly Tyr Gly Ala Ala Ser Tyr Val Ala Pro Thr Phe
 50 55 60

Gly Ala Ala Phe Arg Gln Gln His Leu Asp Leu Leu Asp Tyr Leu Ser
 65 70 75 80

Asp Asp Gln Gly Val Pro Ala Pro Pro Pro Ala Ala Val Pro Ser Ala
 85 90 95

Ser Tyr Val Thr Pro Ala Pro Ala Met Ala Pro Ala Glu Pro Val Val
 100 105 110

Pro Asp Ala Val Ala Ala Ala Gly Gly Tyr Pro Arg Ser Val Ala Ala
 115 120 125

Ala Ala Ala Ala Val Ala Gly Glu Gly Arg Asp Arg Thr Thr Thr Asp
 130 135 140

Lys Ile Ala Phe Arg Thr Arg Ser Asp Asp Glu Ile Leu Asp Asp Gly
145 150 155 160

Tyr Lys Trp Arg Lys Tyr Gly Lys Lys Ser Val Lys Asn Ser Pro Asn
165 170 175

Pro Arg Asn Tyr Tyr Arg Cys Ser Thr Glu Gly Cys Asn Val Lys Lys
180 185 190

Arg Val Glu Arg Asp Lys Asn Asp Pro Arg Tyr Val Val Thr Met Tyr
195 200 205

Glu Gly Ile His Asn His Val Cys Pro Gly Thr Val Tyr Tyr Ala Ala
210 215 220

Gln Asp Ala Ala Ser Gly Arg Phe Phe Val Ala Gly Ile Ser His Pro
225 230 235 240

Asp Leu Asn

<210> 143

<211> 766

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3726 Predicted polypeptide sequence is orthologous to G1274

<400> 143

gatttagcgc caatccttat aaatacggag ctttcgcgcc ggctcgtac tcggccatgg 60

cggcagtcgg cgcgacgca gcggtctacc accacccggt ctcgggcctc tcggcgccgg 120

cgggcgacgc cgctactcg atgtcatcgt acttctccca cgggggaagc tcgacctcca 180

gctccgcgtc cagcttctcc gccgccctcg ccgccgcaac gacgccgccc cttcccagacc 240

cgtcgggggc gcagttcgac atctccgagt tcttcttcga cgacgcgcct ccggccgccc 300

tggttcaatgg cgcgcccacc gccgcgctgc cggatggcgc cgccgcaaac gcaacaagga 360

gcgcggcgga ggcggtgccg gcgccggcgc cggcgggcgt ggagaggccg cggacggagc 420

ggatcgcggt ccggacgaag tcagagatcg agattcttga cgacggctac aagtggcgca 480

agtacggcaa gaagtccgtc aagaacagcc ccaacccaag gaactactac cgggtgctcga 540

cggaaggggtg caacgtgaag aagaggggtg agcgggacaa ggacgacccg agctacgtgg 600

tgacgacgta cgagggggacg cacaaccacg tgagccccag cacggtgtac tacgccagcc 660

aggacgccgc ctccggccgc ttcttcgctcg ccggcacgca gccgccaggt tctctcaatt 720

aaccgcgcgc gtacgggttaa tttgatcgat cgggtcagcc atggga 766

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<210> 144
<211> 221
<212> PRT
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3726 polypeptide Orthologous to G1274

<400> 144

Met Ala Ala Val Gly Ala His Ala Ala Val Tyr His His Pro Val Ser
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Gly Leu Ser Ala Pro Ala Gly Asp Ala Ala Tyr Ser Met Ser Ser Tyr
          20          25          30

Phe Ser His Gly Gly Ser Ser Thr Ser Ser Ser Ala Ser Ser Phe Ser
          35          40          45

Ala Ala Leu Ala Ala Ala Thr Thr Pro Pro Leu Pro Asp Pro Ser Gly
          50          55          60

Ser Gln Phe Asp Ile Ser Glu Phe Phe Phe Asp Asp Ala Pro Pro Ala
65          70          75          80

Ala Val Phe Asn Gly Ala Pro Thr Ala Ala Leu Pro Asp Gly Ala Ala
          85          90          95

Ala Asn Ala Thr Arg Ser Ala Ala Glu Ala Val Pro Ala Pro Ala Pro
          100          105          110

Ala Ala Val Glu Arg Pro Arg Thr Glu Arg Ile Ala Phe Arg Thr Lys
          115          120          125

Ser Glu Ile Glu Ile Leu Asp Asp Gly Tyr Lys Trp Arg Lys Tyr Gly
          130          135          140

Lys Lys Ser Val Lys Asn Ser Pro Asn Pro Arg Asn Tyr Tyr Arg Cys
145          150          155          160

Ser Thr Glu Gly Cys Asn Val Lys Lys Arg Val Glu Arg Asp Lys Asp
          165          170          175

Asp Pro Ser Tyr Val Val Thr Thr Tyr Glu Gly Thr His Asn His Val
          180          185          190

Ser Pro Ser Thr Val Tyr Tyr Ala Ser Gln Asp Ala Ala Ser Gly Arg
          195          200          205

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Phe Phe Val Ala Gly Thr Gln Pro Pro Gly Ser Leu Asn
210 215 220

<210> 145
<211> 1696
<212> DNA
<213> Zea mays

<220>
<223> G3727 Predicted polypeptide sequence is orthologous to G1274

<400> 145
cggacggcac atcaacggac agacacacac aagcaaggcg gctagcgggtg caagtagtgc 60
gaagctagct aggtgctggt gcatgcaatg gcggcttcgc tgggtctgaa ccctgaagct 120
gtcttcactt cctacacctc ctgcgcccg ttcattgtcg actacgtggc ggcgagcttc 180
ctgcgcccg cgcgtcgtga ctccacggac ttctctgcag agctcgatga tcttcaccac 240
cacttggatt actcatcgcc ggccgccgacc ttggccgggg ctccgagcga tcgcagcgag 300
aagcagatga tcaggtggtg tgaggggtgt ggtggcgaga agagactcgg taggatcggg 360
ttcagaacga gatcagaggt ggagatcttg gacgatggat tcaaattggag gaagtatggc 420
aagaaggctg tcaagagtag cccaaatcca aggaactact accgctgctc gtcggagggc 480
tgccggcgtga agaagcgggt ggagagggac cgcgacgacc cccgctacgt catcaccacc 540
tacgacggcg tccacaacca cgcaagcccc gcagccgccg ccatcatcca gtacggcggc 600
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tccttcgtcc tctgacttct ccgggccttg acccagagtg atctgatcta cctgctttat 720
cccagtcgta ggatgagaag agtggttcaga cttcagagac atcagttcag cggccggcta 780
aattcggacc tgattgtaga tatttacacc tcaattattg gttacctctt gtgacgactg 840
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tctttgttcg gtattagacc ccaagatcaa catttacgct gaacagatgc tttgtaacag 1020
tgaaggaata ttttatgggt tttccagata tatgccatta tgaaaataaa aaaaaaaaaa 1080
aaaaaagcgg ccgcttggtt tgtctctttg ttggcattcc ttgcaacaaa ttattaattc 1140
tccacggtag agaacgggac atcatcacia tgtcagtgcg caaccataac tgaactgcaa 1200
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<210> 146
<211> 195
<212> PRT
<213> Zea mays

<220>
<223> G3727 polypeptide Orthologous to G1274

<400> 146

Met Ala Ala Ser Leu Gly Leu Asn Pro Glu Ala Val Phe Thr Ser Tyr
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Thr Ser Ser Pro Pro Phe Met Ser Asp Tyr Val Ala Ala Ser Phe Leu
20 25 30

Pro Pro Ala Val Val Asp Ser Thr Asp Phe Ser Ala Glu Leu Asp Asp
35 40 45

Leu His His His Leu Asp Tyr Ser Ser Pro Ala Pro Thr Leu Ala Gly
50 55 60

Ala Arg Ser Asp Arg Ser Glu Lys Gln Met Ile Arg Trp Cys Glu Gly
65 70 75 80

Gly Gly Gly Glu Lys Arg Leu Gly Arg Ile Gly Phe Arg Thr Arg Ser
85 90 95

Glu Val Glu Ile Leu Asp Asp Gly Phe Lys Trp Arg Lys Tyr Gly Lys
100 105 110

Lys Ala Val Lys Ser Ser Pro Asn Pro Arg Asn Tyr Tyr Arg Cys Ser
115 120 125

Ser Glu Gly Cys Gly Val Lys Lys Arg Val Glu Arg Asp Arg Asp Asp
130 135 140

Pro Arg Tyr Val Ile Thr Thr Tyr Asp Gly Val His Asn His Ala Ser
145 150 155 160

Pro Ala Ala Ala Ala Ile Ile Gln Tyr Gly Gly Gly Gly Gly Phe Tyr
165 170 175

Ser Pro Pro His Ser Gly Ser Pro Ser Ala Ala Ser Tyr Ser Gly Ser
180 185 190

Phe Val Leu
195

<210> 147
<211> 1663
<212> DNA
<213> Zea mays

<220>
<223> G3728 Predicted polypeptide sequence is orthologous to G1274

<400> 147
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gtgatgtatg cagctgaggc atcctaacag accccggccg acgggaaaca agaaagaaaa 120
aatcgagagg acgccagggc cgattctctg cgtgacttgg ggcgctcgctg ccgagttttc 180
tccggccgag ggcgggcgca ccggacaacc agcgtgagcg cgaccggcga catgactcgc 240
ggcaaccagc gtgaccgca ccgtagagcg gcggcgggcg ggaagcccaa cgccaagaac 300
tcccaggacg ggctcacccc ggagcagcgc cgcgagaggg acaagaaagc tctggaggag 360
aaggcggcca agaaggcgca gcaggcagcg gccggcggca ccgggacctc cacggacaac 420
aacaagaaca aggcaggtgg caagaagtag gaggcagtg cgcgccgcca cctctgtacg 480
attaatcgat gccttgagct tgtaacttgt tcgcatacct gtaggtgca tgcttgttgg 540
gtcataaact ctgatgatat cgagatttgg tgatcagaaa taatgcgtgg ttttcgcgcc 600
caaaattggg aaccccgagg ccggccgggg ttattcaggc aggcgcattg actgatacac 660
atatatacaa caagcaaggc ggctagctac agcggctagt gcgcgcgtgg tgcaggcgca 720
tctagctact acctggtgct tgttgtgcat acaatggcga cttcgctggg actgaaccct 780
gaagatctct tcacttcgta ctcgtcttcc tactactcct cgccgccgtt catgtccgac 840
tacgcggcga gcttcacgcc ggcgccgggg gactccacgg ccttctcctc ggagctcgac 900
gaccttcacc acttcgacta ctcaccggcg ccgatcgta ctgctgccgg agccggggct 960
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ggattcaagt ggaggaagta cgggaagaag gccgtcaaga acagcccaa tccaaggaac 1140
tactaccgct gctcgtcgga gggctgcggc gtgaagaagc ggggtggagag ggaccgcgac 1200
gacccccgct acgtcatcac cacctacgac ggcgtccaca accacgccag ccccgagacc 1260
gctgctatca tcgtcccgtg cggcagcggc ggcggaata gcggcttcta cagcccgcg 1320
cacagcggct ccccgtcggc cacctcctac tcgggctccc tagccttctg acttttccgg 1380
gccttgaccc atagttacct ttacactcca gtcgtcggat aagaagaatg ttcagcggct 1440
ggctaaacag tctcaactgc tgcagctatt caaattagtg ttggagatgc aatttataga 1500

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gataaaatac tctagaagct atcgctgtag ccggattaaa ttctgaccta cttgtatagt 1560
 ttacactta cacagtgcaa gtaataatat ttaaggggaag cagagagcac tctaggcggc 1620
 cgctcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aag 1663

<210> 148
 <211> 205
 <212> PRT
 <213> Zea mays

<220>
 <223> G3728 polypeptide Orthologous to G1274

<400> 148

Met Ala Thr Ser Leu Gly Leu Asn Pro Glu Asp Leu Phe Thr Ser Tyr
 1 5 10 15

Ser Ser Ser Tyr Tyr Ser Ser Pro Pro Phe Met Ser Asp Tyr Ala Ala
 20 25 30

Ser Phe Thr Pro Ala Ala Gly Asp Ser Thr Ala Phe Ser Ser Glu Leu
 35 40 45

Asp Asp Leu His His Phe Asp Tyr Ser Pro Ala Pro Ile Val Thr Ala
 50 55 60

Ala Gly Ala Gly Ala Gly Gly Gly Asp Arg Asn Glu Lys Met Met Trp
 65 70 75 80

Cys Glu Gly Gly Gly Asp Glu Arg Arg Leu Arg Ser Asn Gly Arg Ile
 85 90 95

Gly Phe Arg Thr Arg Ser Glu Val Glu Ile Leu Asp Asp Gly Phe Lys
 100 105 110

Trp Arg Lys Tyr Gly Lys Lys Ala Val Lys Asn Ser Pro Asn Pro Arg
 115 120 125

Asn Tyr Tyr Arg Cys Ser Ser Glu Gly Cys Gly Val Lys Lys Arg Val
 130 135 140

Glu Arg Asp Arg Asp Asp Pro Arg Tyr Val Ile Thr Thr Tyr Asp Gly
 145 150 155 160

Val His Asn His Ala Ser Pro Gly Ala Ala Ala Ile Ile Val Pro Tyr
 165 170 175

Gly Ser Gly Gly Gly Asn Ser Gly Phe Tyr Ser Pro Pro His Ser Gly
 180 185 190

Ser Pro Ser Ala Thr Ser Tyr Ser Gly Ser Leu Ala Phe
195 200 205

<210> 149
<211> 1091
<212> DNA
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3729 Predicted polypeptide sequence is orthologous to G1274

<400> 149
aaagcgctct gcgtgagctg agctgagcta ggcgtcgcgc gcgatgtcgt cgctgtaccc 60
gtctctcctc tcgctgagcg agagccccgc cgagtaccgg caggtcggcg gtggccgcta 120
cgcggggggag gacgtcgtcg acgacgacga cgacatgggt gccgtcgccg acgctgtgtc 180
cagctacctc tccttcgaca tggacgacgt cgagtattac acgccggagg tgggcttcca 240
ctcaaagcag cacaaccgc cgccagttgc tgcggcgcca ctggaagccg gaggaggcag 300
ggagcaaagc cggcggggaag ccgccgtcaa tcttggaag atggacaggg gaccggcgcc 360
ggtgagcggc ggcgcggcga ctggcgggcgt gccgaggagc aagaacggca gcaagatcgc 420
gttcaagacg aggtcggagg tggacgtgct ggacgacggc taccggtgga ggaagtacgg 480
caagaagatg gtcaagaaca gcccacaacc aaggaactac taccggtgct cgagcgaggg 540
gtgccgcgtg aagaagcggg tggagcgcgc ccgggacgac gcgcgcttcg tcgtcaccac 600
ctacgacggc gtccacaacc acccggcgcc gctgcacctc aggccgcagc tgccgccgcc 660
cggcggttac tcgatcgccg gggcaccggc cgtggtggcg ccgcacggcc gcctcgggct 720
ggaggaggcc gaggtgatcg ctctcttcag gggcaccacc gccacctcgc tgctgcttcc 780
ttgaccggcc agtccgacgc ggcggcgccg gcggcgacaa ctgactagct agtgtgagtc 840
ctggggccgta caggaatgga caattagttt gtctccgata gaggaccaag gcgacctgaa 900
tcaaaattac ggcccatcga tatatagtag gtcgtttaat tcatcgaaat tagacgaatt 960
tcatgtacaa ttattgcatt acagtattat ttgaaacagt attgtatata ttgctatac 1020
aatttgatgg atcgtatgtc tttagcagtt gtaagtatat taatctatag atctagtagt 1080
tcagccatga t 1091

<210> 150
<211> 246
<212> PRT
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3729 polypeptide Orthologous to G1274

<400> 150

MBI0058CIP.ST25.txt

Met Ser Ser Leu Tyr Pro Ser Leu Leu Ser Leu Ser Glu Ser Pro Ala
1 5 10 15

Glu Tyr Arg Gln Val Gly Gly Gly Arg Tyr Ala Gly Glu Asp Val Val
20 25 30

Asp Asp Asp Asp Asp Met Ala Ala Val Ala Asp Ala Val Ser Ser Tyr
35 40 45

Leu Ser Phe Asp Met Asp Asp Val Glu Tyr Tyr Thr Pro Glu Val Gly
50 55 60

Phe His Ser Lys Gln His Asn Pro Pro Pro Val Ala Ala Ala Pro Leu
65 70 75 80

Glu Ala Gly Gly Gly Arg Glu Gln Ser Arg Arg Glu Ala Ala Val Asn
85 90 95

Leu Gly Lys Met Asp Arg Gly Pro Ala Pro Val Ser Gly Gly Ala Ala
100 105 110

Thr Gly Gly Val Pro Arg Ser Lys Asn Gly Ser Lys Ile Ala Phe Lys
115 120 125

Thr Arg Ser Glu Val Asp Val Leu Asp Asp Gly Tyr Arg Trp Arg Lys
130 135 140

Tyr Gly Lys Lys Met Val Lys Asn Ser Pro Asn Pro Arg Asn Tyr Tyr
145 150 155 160

Arg Cys Ser Ser Glu Gly Cys Arg Val Lys Lys Arg Val Glu Arg Ala
165 170 175

Arg Asp Asp Ala Arg Phe Val Val Thr Thr Tyr Asp Gly Val His Asn
180 185 190

His Pro Ala Pro Leu His Leu Arg Pro Gln Leu Pro Pro Pro Gly Gly
195 200 205

Tyr Ser Ile Ala Gly Ala Pro Ala Val Val Ala Pro His Gly Arg Leu
210 215 220

Gly Leu Glu Glu Ala Glu Val Ile Ala Leu Phe Arg Gly Thr Thr Ala
225 230 235 240

Thr Ser Leu Leu Leu Pro
245

<210> 151
 <211> 850
 <212> DNA
 <213> Oryza sativa (japonica cultivar-group)

<220>
 <223> G3730 Predicted polypeptide sequence is orthologous to G1274

<400> 151
 ctgtcaaaca ctcaatcagc agcagcagca gctagcttag cttagctaac gcacagtgc 60
 gcgagcatgg cggcttcgct gggactctgc cagcagacgt cgtacgccta ctccgtaccg 120
 gcgtcgaaca cctcctcctc cttgtgcttc cctcctctca tggcggacca catcgtcgac 180
 ggcggcgggc gcggcggtg ttcctttggt gaattcctgg agctcggcca ttccgtgtac 240
 tcgctgccgc ttccgccgcc gccgtcgcag ccggtggtgg tcgccggcgg gaacaatgat 300
 cagtatggcg tgcgtcgtc gtcgtcggcg gcggcgacga cgagcaggat cgggttcagg 360
 acgaggtcgg aggtggaggt gctggacgac gggttcaagt ggcgaaagta cgggaagaag 420
 gcggtgaaga gcagcccgaa cccgcggaac tactaccggt gtcggcgggc ggggtgcggc 480
 gtcaagaagc ggggtggagcg cgacggcgac gaccgcgct acgtcgtcac cacctacgac 540
 ggcgtccaca accacgcgac ccccggtgct gtcggcgggc gcggccacct cccgtaccct 600
 acttccgctg cgccgccgtg gagcgttcg gcggcgggcg cctcgccgcc tcccgcgcac 660
 gcgcaggcgt gggggggcgcc gctgcacgcc gccgcggcg cgactcgtc ggaatcgtc 720
 ttctgaacgc tgaatttact tctgtttttg tttttcttgg ttgcttgta gttgtaccgc 780
 cgttcgtgat cgatcgatcg gttcttgtat gcactagact tactacttaa aaaaaaaaaa 840
 gttaaattctt 850

<210> 152
 <211> 219
 <212> PRT
 <213> Oryza sativa (japonica cultivar-group)

<220>
 <223> G3730 polypeptide Orthologous to G1274

<400> 152

Met Ala Ala Ser Leu Gly Leu Cys His Glu Thr Ser Tyr Ala Tyr Ser
 1 5 10 15

Tyr Pro Ala Ser Asn Thr Ser Ser Ser Leu Cys Phe Pro Pro Leu Met
 20 25 30

Ala Asp His Ile Val Asp Gly Gly Gly Gly Gly Gly Cys Ser Phe Gly
 35 40 45

Glu Phe Leu Glu Leu Gly His Ser Val Tyr Ser Leu Pro Leu Pro Pro
 50 55 60

Pro Pro Ser Gln Pro Val Val Val Ala Gly Gly Asn Asn Asp Gln Tyr
65 70 75 80

Gly Val Ser Ser Ser Ser Ser Ala Ala Ala Thr Thr Ser Arg Ile Gly
85 90 95

Phe Arg Thr Arg Ser Glu Val Glu Val Leu Asp Asp Gly Phe Lys Trp
100 105 110

Arg Lys Tyr Gly Lys Lys Ala Val Lys Ser Ser Pro Asn Pro Arg Asn
115 120 125

Tyr Tyr Arg Cys Ser Ala Ala Gly Cys Gly Val Lys Lys Arg Val Glu
130 135 140

Arg Asp Gly Asp Asp Pro Arg Tyr Val Val Thr Thr Tyr Asp Gly Val
145 150 155 160

His Asn His Ala Thr Pro Gly Cys Val Gly Gly Gly Gly His Leu Pro
165 170 175

Tyr Pro Thr Ser Ala Ala Pro Pro Trp Ser Val Pro Ala Ala Ala Ala
180 185 190

Ser Pro Pro Pro Ala His Ala Gln Ala Trp Gly Ala Pro Leu His Ala
195 200 205

Ala Ala Ala Ala His Ser Ser Glu Ser Ser Phe
210 215

<210> 153

<211> 708

<212> DNA

<213> Lycopersicon esculentum

<220>

<223> G3731 Predicted polypeptide sequence is orthologous to G1274

<400> 153

cgttccggttc aactatggaa aattttccct atagctcatc aaaccctaac cctaatttta 60

tcgacgcacg ggagaatttt gagctctccg attataatta tctttttctc gatgatggat 120

cgagtgcacga ttttttgtca caaaatgaaa ttgttcaaag tgtttccgat actagtgggt 180

catattcaaa taatcctact ccaacaagtc ataacataaa atgtatgaaa ggtataaaga 240

agggtggatgc aaagtctaag gttgcattta gatttagatc agagttggag gtgttggatg 300

atggatttaa atgtaggaaa tatggcaaaa agatgggtcaa gaataatcca aatccaagga 360

attactacaa atgttcaagt gggggatgca atgtgaagaa aagagtagaa agggacaata 420

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aagattcaag ctatgtcatt actacttatg aagggattca caaccacgag agtcctcatg      480
tgcttcacta cacacaattc cctcccaaca atattgccct tcacaatctt cacctttaga      540
acctcttaaa cgtgtcagta aagtttagtt atatatttgt attatggtag gttctaattg      600
agcactttga ttatatgata aagtgttttt attgaacatt ttcgacatat gttttaaaaa      660
agttgtgcac gaattttcaa gtgctaaata tatagataag ttaatcgc                    708

```

```

<210> 154
<211> 174
<212> PRT
<213> Lycopersicon esculentum

```

```

<220>
<223> G3731 polypeptide Orthologous to G1274

```

```

<400> 154

```

```

Met Glu Asn Phe Pro Tyr Ser Ser Ser Asn Pro Asn Pro Asn Phe Ile
1          5          10          15

```

```

Asp Ala Ser Glu Asn Phe Glu Leu Ser Asp Tyr Asn Tyr Leu Phe Leu
20          25          30

```

```

Asp Asp Gly Ser Ser Asp Asp Phe Leu Ser Gln Asn Glu Ile Val Gln
35          40          45

```

```

Ser Val Ser Asp Thr Ser Gly Ser Tyr Ser Asn Asn Pro Thr Pro Thr
50          55          60

```

```

Ser His Asn Ile Lys Cys Met Lys Gly Ile Lys Lys Val Asp Ala Lys
65          70          75          80

```

```

Ser Lys Val Ala Phe Arg Phe Arg Ser Glu Leu Glu Val Leu Asp Asp
85          90          95

```

```

Gly Phe Lys Cys Arg Lys Tyr Gly Lys Lys Met Val Lys Asn Asn Pro
100         105         110 /

```

```

Asn Pro Arg Asn Tyr Tyr Lys Cys Ser Ser Gly Gly Cys Asn Val Lys
115         120         125

```

```

Lys Arg Val Glu Arg Asp Asn Lys Asp Ser Ser Tyr Val Ile Thr Thr
130         135         140

```

```

Tyr Glu Gly Ile His Asn His Glu Ser Pro His Val Leu His Tyr Thr
145         150         155         160

```

```

Gln Phe Pro Pro Asn Asn Ile Ala Leu His Asn Leu His Leu
165         170

```

<210> 155
 <211> 743
 <212> DNA
 <213> Solanum tuberosum

<220>
 <223> G3732 Predicted polypeptide sequence is orthologous to G1274

<400> 155
 tttctatctt ttctttccct tcaacaatgg aaaattttcc atatagctca tcaaacccta 60
 accctaattt catcgatgca tcggagaatt ttgagctctc agattataat tatctctttc 120
 ttgatgatgg atcaaatgac gattttttgt cacaaaatga aattgttcaa agtgtttccg 180
 atagtagtgg atcatattca aataatccca ctccaacaag tcataacata aaatgtatga 240
 aaggtgtaaa gaaggtggat gcaaagtcta gggttgcatt tagatttaga tcagagttgg 300
 aggtgttgga tgatggattt aaatggagga aatatggcaa aaagatggtc aagaatagtt 360
 caaatccaag gaattactac aaatgttcaa gtggaggatg caatgtgaag aaaagagtag 420
 aaagggacaa tgaagattca agctatgtca ttactactta tgaagggatt cacaaccatg 480
 agagtcctta tgtgtttcac tacacacaat tccctcccaa caatattgcc cttcacaatc 540
 tttgccttta gaacctctta aacgtgtcag taaatttcag ttatatattt gtataatggg 600
 aggttctaata agagcacttt gatcatatga taaagtgttt ctattaaaca ttttcgactt 660
 atgttttaaa aaaatgtgtg cacgtgtttt caagtgcccg atatatagat aagttaatca 720
 cataaaatat gtctctttct ttg 743

<210> 156
 <211> 174
 <212> PRT
 <213> Solanum tuberosum

<220>
 <223> G3732 polypeptide Orthologous to G1274

<400> 156
 Met Glu Asn Phe Pro Tyr Ser Ser Ser Asn Pro Asn Pro Asn Phe Ile
 1 5 10 15
 Asp Ala Ser Glu Asn Phe Glu Leu Ser Asp Tyr Asn Tyr Leu Phe Leu
 20 25 30
 Asp Asp Gly Ser Asn Asp Asp Phe Leu Ser Gln Asn Glu Ile Val Gln
 35 40 45
 Ser Val Ser Asp Ser Ser Gly Ser Tyr Ser Asn Asn Pro Thr Pro Thr
 50 55 60

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Ser His Asn Ile Lys Cys Met Lys Gly Val Lys Lys Val Asp Ala Lys
65 70 75 80

Ser Arg Val Ala Phe Arg Phe Arg Ser Glu Leu Glu Val Leu Asp Asp
85 90 95

Gly Phe Lys Trp Arg Lys Tyr Gly Lys Lys Met Val Lys Asn Ser Ser
100 105 110

Asn Pro Arg Asn Tyr Tyr Lys Cys Ser Ser Gly Gly Cys Asn Val Lys
115 120 125

Lys Arg Val Glu Arg Asp Asn Glu Asp Ser Ser Tyr Val Ile Thr Thr
130 135 140

Tyr Glu Gly Ile His Asn His Glu Ser Pro Tyr Val Phe His Tyr Thr
145 150 155 160

Gln Phe Pro Pro Asn Asn Ile Ala Leu His Asn Leu Cys Leu
165 170

<210> 157
<211> 1387
<212> DNA
<213> Hordeum vulgare

<220>
<223> G3733 Predicted polypeptide sequence is orthologous to G1274

<400> 157
gaattcggca ccagggcgct caccatcgcc gaagcttctc agcgcgaagc tcaccgggaa 60
gccgaccaa atccccggg aaaaaaagag agctctcacg gccggcgcca tctccaacta 120
gtacaaatct acccgccaaa tccactcccc aaccgaatcc atgcagcagc agcagcagca 180
gcgcaccggc gatttagggg gtcttatata ttataaatag gaagcgctct cgccggtgac 240
aaactcggtc atggcggcag tcggagcggc accagtgtct taccaacagc aggcgcaggc 300
ggtgggcgac gcctgttctt tctctccat gtctctctac ttctccaacg aggcaatcag 360
ctctctctgc tccagcccag cctccagctt ctccgcgcgc ctgggcgcca cgccgcccgc 420
tgcccgggcg atcagccccg acccgcgctc gcagttcgac atctccgagt acctctacgg 480
cgacggcccc ttagccgcgc cgctggcgcc cgttggcgct gctgttgcaa gctcggcgac 540
tgcggtgcct gcgaggagcg cggccgagtc ggcggcgggc gtggagaggc cgcgacgga 600
gcgcacgcgc ttccgcacga ggacggagat cgagatctc gacgacggct acaagtggcg 660
caagtacggc aagaagtccg tcaagaacag cccaaaccca aggaactact accggtgtct 720
gacggaaggg tgcagcgtga agaagcgggt ggagcgggac cgggacgacc cggcgtacgt 780
ggtgaccacg tacgagggca cgcacagcca cgccagcccc agcaccgtct actacgccag 840

```

ccaggacgcc gcctccggcc gcttcttcgt cgccggcacg caccgcgcgc caggctccct 900
caactgagta gactagccac caacgacgga gcacgtcgag atcagcacgt acggggcttc 960
catcttgggc aagctagcca gctcgggcct cggtgccgta gcagccacaa gttcgtagtt 1020
aaactagtgc actactggtt caggttcggg ttcccgactg tagtggttggt tactgcgggtg 1080
tgcactgtcg gctcgatcac cagggttttat ccctcgagca taattagtgg atcgaaagag 1140
cccggccggg gaacgtaact cagtccacta ctagtgctgc ctacttaacc gtgtaataaa 1200
aatacccatg tgcggtttcc ctcagcccat aggcctccga gagttccatg ttaagcacc 1260
aacatgcata aaagagcata taaaaaaagc atcaaagaga tccatgtaga aaaagtttgt 1320
cgtattaccc gacagaaaaa agtttgtagc atttttttgg taaataattt tggaagggtt 1380
tacagtt 1387

```

```

<210> 158
<211> 218
<212> PRT
<213> Hordeum vulgare

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```

<220>
<223> G3733 polypeptide Orthologous to G1274

```

```

<400> 158

```

```

Met Ala Ala Val Gly Ala Ala Pro Val Leu Tyr Gln Gln Gln Ala Gln
1          5          10          15

```

```

Ala Val Gly Asp Ala Cys Phe Phe Ser Ser Met Ser Ser Tyr Phe Ser
          20          25          30

```

```

Asn Glu Ala Ile Ser Ser Ser Cys Ser Ser Pro Ala Ser Ser Phe Ser
          35          40          45

```

```

Ala Ala Leu Gly Ala Thr Pro Pro Ala Ala Pro Ala Ile Ser Pro Asp
          50          55          60

```

```

Pro Ala Ser Gln Phe Asp Ile Ser Glu Tyr Leu Tyr Gly Asp Gly Pro
65          70          75          80

```

```

Leu Ala Ala Pro Leu Ala Pro Val Gly Ala Ala Val Ala Ser Ser Ala
          85          90          95

```

```

Thr Ala Val Pro Ala Arg Ser Ala Ala Glu Ser Ala Ala Ala Val Glu
          100          105          110

```

```

Arg Pro Arg Thr Glu Arg Ile Ala Phe Arg Thr Arg Thr Glu Ile Glu
          115          120          125

```


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Ile Leu Asp Asp Gly Tyr Lys Trp Arg Lys Tyr Gly Lys Lys Ser Val
130 135 140

Lys Asn Ser Pro Asn Pro Arg Asn Tyr Tyr Arg Cys Ser Thr Glu Gly
145 150 155 160

Cys Ser Val Lys Lys Arg Val Glu Arg Asp Arg Asp Asp Pro Ala Tyr
165 170 175

Val Val Thr Thr Tyr Glu Gly Thr His Ser His Ala Ser Pro Ser Thr
180 185 190

Val Tyr Tyr Ala Ser Gln Asp Ala Ala Ser Gly Arg Phe Phe Val Ala
195 200 205

Gly Thr His Pro Pro Pro Gly Ser Leu Asn
210 215

<210> 159
<211> 653
<212> DNA
<213> Medicago truncatula

<220>
<221> misc_feature
<222> (605)..(605)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (610)..(610)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (615)..(615)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (625)..(625)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (647)..(647)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (652)..(652)
<223> n is a, c, g, or t

<220>
<223> G3735 Predicted polypeptide sequence is orthologous to G1792

<400> 159

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ctaatecttc atactaaaga aaacatagac ttataacaaa aatattatta ttacttcgt      60
atatttttgt gtttcaaatt aatggaggga gatcataaat tagtttcaaa ttcaacaaat    120
ggaaatggaa atggaaatgg aaattcagat caaataaagt atagaggaat tcgtagaaga    180
ccatgggggaa aatttgcagc agaaattcgt gacccaacaa ggaaagggac aagaatatgg   240
cttggacat  ttgatactgc tgaacaagct gcaagagctt atgatgctgc tgcttttcat    300
tttcgtgggc atagagctat tctcaatttc cctaataaat atcaagctcc taattcatct    360
tcttcattac ctatgcctct tactatgcct ccaccacctt cttctaatacc acctccttct   420
tcttcttctt cttcctcttt ttcttcttac accgttgatg atggttttga tgagcttgaa   480
ttcttggata ataagttgct tcaagaactt cttcaagatg gaacacaata gttaactatt    540
gaagatcaag tggcatgaaa tgtattggtg gtcatttaaat tttctcttca ttaattttatt   600
ttggnttggn tatgnatctc atttntatga ataaatgaga atgggggnatt ana          653

```

<210> 160

<211> 149

<212> PRT

<213> Medicago truncatula

<220>

<223> G3735 polypeptide Orthologous to G1792

<400> 160

```

Met Glu Gly Asp His Lys Leu Val Ser Asn Ser Thr Asn Gly Asn Gly
1           5           10           15

```

```

Asn Gly Asn Gly Asn Ser Asp Gln Ile Lys Tyr Arg Gly Ile Arg Arg
20           25           30

```

```

Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile Arg Asp Pro Thr Arg Lys
35           40           45

```

```

Gly Thr Arg Ile Trp Leu Gly Thr Phe Asp Thr Ala Glu Gln Ala Ala
50           55           60

```

```

Arg Ala Tyr Asp Ala Ala Ala Phe His Phe Arg Gly His Arg Ala Ile
65           70           75           80

```

```

Leu Asn Phe Pro Asn Glu Tyr Gln Ala Pro Asn Ser Ser Ser Ser Leu
85           90           95

```

```

Pro Met Pro Leu Thr Met Pro Pro Pro Pro Ser Ser Asn Pro Pro Pro
100          105          110

```

```

Ser Ser Ser Ser Ser Ser Ser Phe Ser Ser Tyr Thr Val Asp Asp Gly
115          120          125

```

Phe Asp Glu Leu Glu Phe Leu Asp Asn Lys Leu Leu Gln Glu Leu Leu
 130 135 140

Gln Asp Gly Thr Gln
 145

<210> 161
 <211> 859
 <212> DNA
 <213> Triticum aestivum

<220>
 <223> G3736 Predicted polypeptide sequence is orthologous to G1792

<400> 161
 gcacgaggct tcattctccc tcgttccatc caagctccac catccatcac tgatttgcac 60
 ttacctagct actccgcaac cccacttcc ggcttcttca tttctcacta ctagtacgta 120
 gttgagatta tggagggcgg agaaggatcc ggtggcggcg gcgagccgac caagtaccgc 180
 ggggtgcgcc gcaggccgtg gggcaagttc gccgcggaga tccgggactc gagccggcac 240
 ggcgtgcgca tgtggctcgg caccttcgac accgccgagg aggccgcggc cgcctacgac 300
 cgctccgcct actccatgcg cggccgcaac gccgtgctca acttccccga ccgggcgcac 360
 gtctacgagg ccgaggccag gcgccagggc cagggctctt cgtcgtcggc gaggcagcag 420
 aatcagcagc agcagcaggg gcagagcggg gtgatcgagt tcgagtacct ggacgacgac 480
 gtgctgcagt ccatgctcca cgaccacgac aaatccaaca agtagatcga tggatcatcc 540
 atccatccat ccatggatcg atccataata cctactgtat catcccggcc cggccggcaa 600
 catcgacctg cgtgcatgcg cgggcgcgga tgcaatctac actacctacc tatgcattcc 660
 ggccatatat taggtacgta gattatatgt gtacgagagc ctacgagctc gatgaagatc 720
 gtacgtgggtg cattctgatg catgaggatt ccatcgacac gacctctac catatatattg 780
 atgggtcgat cgagtaattt gcagccagta atccaatcga tgatatgggg ttttcaaaaa 840
 aaaaaaaaaa aaaaaaaaaa 859

<210> 162
 <211> 131
 <212> PRT
 <213> Triticum aestivum

<220>
 <223> G3736 polypeptide Orthologous to G1792

<400> 162

Met Glu Gly Gly Glu Gly Ser Gly Gly Gly Glu Pro Thr Lys Tyr
 1 5 10 15

Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile Arg
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20

25

30

Asp Ser Ser Arg His Gly Val Arg Met Trp Leu Gly Thr Phe Asp Thr
 35 40 45

Ala Glu Glu Ala Ala Ala Ala Tyr Asp Arg Ser Ala Tyr Ser Met Arg
 50 55 60

Gly Arg Asn Ala Val Leu Asn Phe Pro Asp Arg Ala His Val Tyr Glu
 65 70 75 80

Ala Glu Ala Arg Arg Gln Gly Gln Gly Ser Ser Ser Ser Ala Arg Gln
 85 90 95

Gln Asn Gln Gln Gln Gln Gln Gly Gln Ser Gly Val Ile Glu Phe Glu
 100 105 110

Tyr Leu Asp Asp Asp Val Leu Gln Ser Met Leu His Asp His Asp Lys
 115 120 125

Ser Asn Lys
 130

<210> 163
 <211> 882
 <212> DNA
 <213> *Oryza sativa* (japonica cultivar-group)

<220>
 <223> G3737 Predicted polypeptide sequence is orthologous to G1792

<400> 163
 acacatgcat cgatcattca tggatgccga attgccgcga tccgggcatt atttcgcgcc 60
 aggagaccca agatcatcgt gtcgcccacg ctataaatag ctagctagct tgcctttatg 120
 ttgcatatgc caactgctac atgcaggacg tctgaaacta tcattagtga cctgcagcgc 180
 ctgcagtata tatatacaag tagtagtgag catggaggac gacaagaagg aggcggcgag 240
 caagtaccgc ggcgtacgga ggcggccgtg gggcaaattc gcggcgagaga tccgcgaccc 300
 ggagcgcggc ggctcacgcg tctggcttgg cacgttcgac accgccgagg aggccgcgcg 360
 agcgtacgac cgcgccgcat tcgccatgaa gggcgctatg gccgtgctca acttcccagg 420
 caggacgagc agcaccggct cttcgtcgtc atcgtcatcc acgccgccag ctccggtgac 480
 gacgagccgc cactgcgccg acacgacgga gaaggtggag cttgtgtacc ttgacgacaa 540
 ggtgctcgac gagctccttg cggaggacta cagctaccgc aacaacaaca actactgatc 600
 cggccgtcga tgaactgaga cggatcgaca tggggccggt cgtcggtacg ctcgctgaaa 660
 cgagacccgg attgctatca ataagcaagc agaagaaaac cgtctcctat atatagcttc 720

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ttctgttggc acaagcatat atgggcatgc atgacacatg ctactgtgaa ttgacgggtg 780
 tgtgctgtgt gcagactact aaaccacgct tgcaagttgc acgtacgacg tggttgtcaa 840
 gagcatgcag tccacgaagc agagaaaaac acctggttta tc 882

<210> 164
 <211> 128
 <212> PRT
 <213> Oryza sativa (japonica cultivar-group)

<220>
 <223> G3737 polypeptide Orthologous to G1792

<400> 164

Met Glu Asp Asp Lys Lys Glu Ala Ala Ser Lys Tyr Arg Gly Val Arg
 1 5 10 15

Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile Arg Asp Pro Glu Arg
 20 25 30

Gly Gly Ser Arg Val Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala
 35 40 45

Ala Arg Ala Tyr Asp Arg Ala Ala Phe Ala Met Lys Gly Ala Met Ala
 50 55 60

Val Leu Asn Phe Pro Gly Arg Thr Ser Ser Thr Gly Ser Ser Ser Ser
 65 70 75 80

Ser Ser Ser Thr Pro Pro Ala Pro Val Thr Thr Ser Arg His Cys Ala
 85 90 95

Asp Thr Thr Glu Lys Val Glu Leu Val Tyr Leu Asp Asp Lys Val Leu
 100 105 110

Asp Glu Leu Leu Ala Glu Asp Tyr Ser Tyr Arg Asn Asn Asn Asn Tyr
 115 120 125

<210> 165
 <211> 899
 <212> DNA
 <213> Zea mays

<220>
 <223> G3739 Predicted polypeptide sequence is orthologous to G1792

<400> 165

cgatataatt cactcctctc aacgctcgct gcacacacac accagtgaac ctagccagcc 60

atttgccgca tcgatcatca gtcgctgtca cgcgcgccaa accaaaccaa agcccaaacc 120

cagctgcaag tgctactgac agcagctagc aaacacacac ccgctcgccat cgctatggac 180

MBI0058CIP.ST25.txt

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ggcgactggt ccaaggacgg cggaggtgga gagccgacca aatatcgcg cgtgcggcgg 240
gggccctggg gcaagtacgc ggccgagatc cgcgactcga gccgccacgg cgtccgcatc 300
tggttgggca ctttcgacac cgccgaggag gccgccaggg cgtacgaccg gagcgcttac 360
tccatgcgcg gcgccaacgc cgtcctcaac ttcccggagg acgcgcacgc ctacgccgcc 420
gcttgcgcg gctccggatc ctctcatcc tcgtccaggc ataggcagca gcagcagcag 480
gggtccggca gggacgtgat cgagctcgag tacctcgacg acgaggtgct gcaggagatg 540
ctcaggaacc acgagccgctc gtcgtctgcg aggaagaaga tgtaatgcaa gacgactggt 600
acacgtggcg aatgcacgtt gcacatcaga atgccatgta tgcgtggggg gttacgttca 660
attgtatgca tgcagtgcag tgactaccgg ccggctctcc tggatatgtc ggccatctct 720
ctctatatat tattaataatg tcagctccct tctctaattt ggcgggagtt acatcagtgg 780
tactatgcag agttgcatac ttgcatatat atgcacatta ttaattaata actcgatctc 840
tcgtggacgg tggaacagtg ataatcatct cattgtcaat taattttgat caaagaaat 899

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<210> 166
 <211> 136
 <212> PRT
 <213> Zea mays

<220>
 <223> G3739 polypeptide Orthologous to G1792

<400> 166

Met Asp Gly Asp Trp Ser Lys Asp Gly Gly Gly Gly Glu Pro Thr Lys
 1 5 10 15

Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Tyr Ala Ala Glu Ile
 20 25 30

Arg Asp Ser Ser Arg His Gly Val Arg Ile Trp Leu Gly Thr Phe Asp
 35 40 45

Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Arg Ser Ala Tyr Ser Met
 50 55 60

Arg Gly Ala Asn Ala Val Leu Asn Phe Pro Glu Asp Ala His Ala Tyr
 65 70 75 80

Ala Ala Ala Cys Arg Gly Ser Gly Ser Ser Ser Ser Ser Arg His
 85 90 95

Arg Gln Gln Gln Gln Gln Gly Ser Gly Arg Asp Val Ile Glu Leu Glu
 100 105 110

Tyr Leu Asp Asp Glu Val Leu Gln Glu Met Leu Arg Asn His Glu Pro

Ser Ser Ser Ala Arg Lys Lys Met
130 135

<210> 167
<211> 645
<212> DNA
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3740 Predicted polypeptide sequence is orthologous to G3086

<400> 167
atggccagca acggctttcc aggctcaaaa ggcgggggag gcagcggagc cgaagcccac 60
caccaccctt ccatggccgg cagcggcagc ggcagcagca gcggcgggag gaagatgaag 120
tcccagctga gcttcacggc cgggccgccc cacctctcgc acatcgcgga ggacggcgcc 180
ttccccgacc gcgcggcgcc cgaggcctcc gtgccccgca ccttctccgc cggcggcagc 240
agcggcggcg gcgggttctc catcgtcggg ccgtgggagg agtccaggga catcatctcc 300
accctcggcg ggtacgagtc ccagttcggc ggcattggcg gcacgtcggc gctggagatg 360
gccggcatgg acaggtacct gcagctgcag catgaccagg tgcggttcaa agtgcgggcc 420
aagcgcggct gcgcgacgca ccccaggagc atcgcggaga gggaaacggag gacgagaatt 480
agcgagaagc tcaggaagct gcaggagctg gtgccaaca tggacaagca aacaagcaca 540
gcggacatgt tggaccttgc agttgagcac atcaagggtc tgcagagcca gctgcaggct 600
ctgaagcatg agcaggagaa gtgcacttgc tgcagcaggc cttga 645

<210> 168
<211> 214
<212> PRT
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3740 polypeptide Orthologous to G3086

<400> 168

Met Ala Ser Asn Gly Phe Pro Gly Ser Lys Gly Gly Gly Gly Ser Gly
1 5 10 15

Ala Glu Ala His His His Pro Ser Met Ala Gly Ser Gly Ser Gly Ser
20 25 30

Ser Ser Gly Gly Arg Lys Met Lys Ser Gln Leu Ser Phe Thr Ala Gly
35 40 45

Pro Pro His Leu Ser His Ile Ala Glu Asp Gly Ala Phe Pro Asp Arg
50 55 60

Ala Gly Ala Glu Ala Ser Val Pro Arg Thr Phe Ser Ala Gly Gly Ser
65 70 75 80

Ser Gly Gly Gly Gly Phe Ser Ile Val Gly Pro Trp Glu Glu Ser Arg
85 90 95

Asp Ile Ile Ser Thr Leu Gly Gly Tyr Glu Ser Gln Phe Gly Gly Met
100 105 110

Ala Ser Thr Ser Ala Leu Glu Met Ala Gly Met Asp Arg Tyr Leu Gln
115 120 125

Leu Gln His Asp Gln Val Pro Phe Lys Val Arg Ala Lys Arg Gly Cys
130 135 140

Ala Thr His Pro Arg Ser Ile Ala Glu Arg Glu Arg Arg Thr Arg Ile
145 150 155 160

Ser Glu Lys Leu Arg Lys Leu Gln Glu Leu Val Pro Asn Met Asp Lys
165 170 175

Gln Thr Ser Thr Ala Asp Met Leu Asp Leu Ala Val Glu His Ile Lys
180 185 190

Gly Leu Gln Ser Gln Leu Gln Ala Leu Lys His Glu Gln Glu Lys Cys
195 200 205

Thr Cys Cys Ser Arg Pro
210

<210> 169
<211> 1110
<212> DNA
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3741 Predicted polypeptide sequence is orthologous to G3086

<400> 169
atgaacccgg cgccgtcgag ggcgccgcag cggcagcagc gcggagggga gatgtcggcg 60
cgctacggcg gcgggctgca gttcttcgct gacgccccgc cggcgggggt ggaggggggc 120
gccgcgaccg cgcggaaggt cttcccggtg ccgggcgggg gaggggagca gcagccgccg 180
gagcgcgcca tgaggcagca gcactacggc ggcggcggga gtggtgcggc cgagatctcg 240
ctggggcacg gccacggcca cggcggaag caccatttcc atcagttcgg cgtcgaggcg 300
aaggacgggtg gcggcgccg cgaccagtcg gggtttctga cgcggcaca cagctcgcc 360
cccgggttct tctcgagccc cgtcatggac aacggtttct catcgagtgc tagaccagca 420

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ggatcatcac tcggtgaggt tcgccatggc gccatgagca gcagcagcaa caacaacaag 480
aagatgaagg cccactgag cttcgctagc agcaggcagg gctccggcgg cctctcccag 540
atatccgagg acggcatccc ggacctcact gacagcatcc atggcgccgc tcatcatcat 600
gggcgctccg aggagaacgt ctccaccac gaccacgtcg tccgctcctt ctctccgggt 660
gggttctcga tcgggtcatg ggaggactcc aactccatcg tgttctccac gtcgacgggc 720
aaatcaggag cgcacggcaa cgacgacatc atcgccaccc ctagcaacta cgaatctcag 780
cttggtgcgc ccaggagat ggctggcgta gagaaatacc tgcagatgca gcacgaccag 840
gtgccattca gactacgggc caagcgtgga tgcgcgacgc acccacggag catcgcagag 900
agggagagaa gaacgaggat cagcgagaag ctcaggaagt tgcaggccct ggtgccaac 960
atggacaagc aaacgagtac ttcagacatg ctggacttag cagttgatca catcaaggga 1020
ctgcagagcc agctgcagac tctgaaggaa gacaaggaga aatgcacctg cagctgcaag 1080
caagcatcaa ggaacagacc agccgactaa 1110

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<210> 170
 <211> 369
 <212> PRT
 <213> Oryza sativa (japonica cultivar-group)

<220>
 <223> G3741 polypeptide Orthologous to G3086

<400> 170

Met Asn Pro Ala Pro Ser Arg Ala Pro Gln Arg Gln Gln Arg Gly Gly
 1 5 10 15

Glu Met Ser Ala Arg Tyr Gly Gly Gly Leu Gln Phe Phe Ala Asp Ala
 20 25 30

Pro Pro Ala Gly Val Glu Gly Gly Ala Ala Thr Ala Arg Thr Phe Phe
 35 40 45

Pro Val Pro Gly Gly Gly Gly Glu Gln Gln Pro Pro Glu Arg Ala Met
 50 55 60

Arg Gln Gln His Tyr Gly Gly Gly Gly Ser Gly Ala Ala Glu Ile Ser
 65 70 75 80

Leu Gly His Gly His Gly His Gly Gly Lys His His Phe His Gln Phe
 85 90 95

Gly Val Glu Ala Lys Asp Gly Gly Gly Gly Gly Asp Gln Ser Gly Phe
 100 105 110

Leu Thr Arg His Asn Ser Ser Pro Pro Gly Phe Phe Ser Ser Pro Val

115

120

125

Met Asp Asn Gly Phe Ser Ser Ser Ala Arg Pro Ala Gly Ser Ser Leu
 130 135 140

Gly Glu Val Arg His Gly Ala Met Ser Ser Ser Ser Asn Asn Asn Lys
 145 150 155 160

Lys Met Lys Ala Pro Leu Ser Phe Ala Ser Ser Arg Gln Gly Ser Gly
 165 170 175

Gly Leu Ser Gln Ile Ser Glu Asp Gly Ile Pro Asp Leu Thr Asp Ser
 180 185 190

Ile His Gly Ala Ala His His His Gly Arg Ser Glu Glu Asn Val Ser
 195 200 205

Thr His Asp His Val Val Arg Ser Phe Ser Ser Gly Gly Phe Ser Ile
 210 215 220

Gly Ser Trp Glu Asp Ser Asn Ser Ile Val Phe Ser Thr Ser Thr Gly
 225 230 235 240

Lys Ser Gly Ala His Gly Asn Asp Asp Ile Ile Ala Thr Pro Ser Asn
 245 250 255

Tyr Glu Ser Gln Leu Val Ala Pro Arg Glu Met Ala Gly Val Glu Lys
 260 265 270

Tyr Leu Gln Met Gln His Asp Gln Val Pro Phe Arg Val Arg Ala Lys
 275 280 285

Arg Gly Cys Ala Thr His Pro Arg Ser Ile Ala Glu Arg Glu Arg Arg
 290 295 300

Thr Arg Ile Ser Glu Lys Leu Arg Lys Leu Gln Ala Leu Val Pro Asn
 305 310 315 320

Met Asp Lys Gln Thr Ser Thr Ser Asp Met Leu Asp Leu Ala Val Asp
 325 330 335

His Ile Lys Gly Leu Gln Ser Gln Leu Gln Thr Leu Lys Glu Asp Lys
 340 345 350

Glu Lys Cys Thr Cys Ser Cys Lys Gln Ala Ser Arg Asn Arg Pro Ala
 355 360 365

Asp

<210> 171
 <211> 837
 <212> DNA
 <213> Oryza sativa (japonica cultivar-group)

<220>
 <223> G3742 Predicted polypeptide sequence is orthologous to G3086

<400> 171
 atgggttccg ccatggcggg actctaccgc accgtcagct ccggcggcac ggagtccacc 60
 gccgccgccg ccggcaacag cctcctccgg cagagcagct ccccgccggg cttcctcaac 120
 catcttacca tggacaacgg atacgggaat atgctaagag cgggcatggg cggcggcggc 180
 ggtggcggcg acccgcggtt caaggggcag ctcagcttct cgtcgcggca ggggtcggtg 240
 atgtcccaga tctcggagat gggcagcgag gacgaggagc tcgccggcgg cggcggcagc 300
 ccggaggctg gcagcaacgg cgggtggcgcc gcacgcggcg gctacggcgg cgggtacgcg 360
 atgggggtcct ccgcctggga ggagccctcg ccgccggcga cgtcgtctct cccggacagc 420
 agcctcccgt ccaagcgccc ccgcgacgac ctgccgcggc agctcagcct cccggcggcg 480
 tccaagaaca gcagcaagcc cccctcctcc gcctccgccg ccgcgtcgcc ggagatggcc 540
 gccatcgaga agttcctcca gttccaggac gccgtccctt gcaagatccg cgccaagcgc 600
 ggctgcgcca cccacccccg cagcatcgcc gagcgggtga ggaggacgcg gatcagcgag 660
 cggatacgga agctgcagga gctcgtcccc aacatggaaa agcaaacc aa cactgctgac 720
 atgttggate ttgccgtgga ctacatcaag gagctccaga agcaggtcaa ggtgttaa ac 780
 gacagccggt ccagctgcac ctgctcggcg agcaagcaga agcacttcgc cggctaa 837

<210> 172
 <211> 278
 <212> PRT
 <213> Oryza sativa (japonica cultivar-group)

<220>
 <223> G3742 polypeptide Orthologous to G3086

<400> 172

Met Ala Ser Ala Met Ala Gly Leu Tyr Arg Thr Val Ser Ser Gly Gly
 1 5 10 15

Thr Glu Ser Thr Ala Ala Ala Ala Gly Asn Ser Leu Leu Arg Gln Ser
 20 25 30

Ser Ser Pro Ala Gly Phe Leu Asn His Leu Thr Met Asp Asn Gly Tyr
 35 40 45

Gly Asn Met Leu Arg Ala Gly Met Gly Gly Gly Gly Gly Gly Gly Asp

50
 55
 60
 Pro Arg Leu Lys Gly Gln Leu Ser Phe Ser Ser Arg Gln Gly Ser Val
 65 70 75 80
 Met Ser Gln Ile Ser Glu Met Gly Ser Glu Asp Glu Glu Leu Ala Gly
 85 90 95
 Gly Gly Gly Ser Pro Glu Ala Gly Ser Asn Gly Gly Gly Ala Ala Arg
 100 105 110
 Gly Gly Tyr Gly Gly Gly Tyr Ala Met Gly Ser Ser Ala Trp Glu Glu
 115 120 125
 Pro Ser Pro Pro Ala Thr Ser Leu Leu Pro Asp Ser Ser Leu Pro Ser
 130 135 140
 Lys Arg Pro Arg Asp Asp Leu Pro Arg Gln Leu Ser Leu Pro Ala Ala
 145 150 155 160
 Ser Lys Asn Ser Ser Lys Pro Pro Ser Ser Ala Ser Ala Ala Ala Ser
 165 170 175
 Pro Glu Met Ala Ala Ile Glu Lys Phe Leu Gln Phe Gln Asp Ala Val
 180 185 190
 Pro Cys Lys Ile Arg Ala Lys Arg Gly Cys Ala Thr His Pro Arg Ser
 195 200 205
 Ile Ala Glu Arg Val Arg Arg Thr Arg Ile Ser Glu Arg Ile Arg Lys
 210 215 220
 Leu Gln Glu Leu Val Pro Asn Met Glu Lys Gln Thr Asn Thr Ala Asp
 225 230 235 240
 Met Leu Asp Leu Ala Val Asp Tyr Ile Lys Glu Leu Gln Lys Gln Val
 245 250 255
 Lys Val Leu Asn Asp Ser Arg Ser Ser Cys Thr Cys Ser Ala Ser Lys
 260 265 270
 Gln Lys His Phe Ala Gly
 275

<210> 173
 <211> 450
 <212> DNA
 <213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3744 Predicted polypeptide sequence is orthologous to G3086

<400> 173

```

atgagctccg ggtgggagga gtcgtcgctc atgtcggaca cgaacatctc cggcgtgaag      60
cgccagcgcg actcgtcgga gccgtcccag aacggcggcg gcggcgggcg cctggcgcac      120
cagttcagcc tgccgaagac ctcgtcggag atggcggcca tcgagaagtt cctccagttc      180
caggacgcgg tgccctgcaa gatccgcgcc aagcgcggct gcgccacgca cccgcgcagc      240
atcgccgagc ggggtgaggag gacaaggatc agcgagcgaa tcaggaagct gcaagaactc      300
gtgccaaaca tggacaagca aaccaacact gctgacatgc tggatttggc tgttgactac      360
atcaaggatc ttcagaagca ggtcaaggga ttaaacgaca gccgagctaa ctgcacctgc      420
tcagcgaagc atcagcagta ctctggctag      450

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<210> 174

<211> 149

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3744 polypeptide Orthologous to G3086

<400> 174

```

Met Ser Ser Gly Trp Glu Glu Ser Ser Leu Met Ser Asp Thr Asn Ile
1           5           10           15

```

```

Ser Gly Val Lys Arg Gln Arg Asp Ser Ser Glu Pro Ser Gln Asn Gly
          20           25           30

```

```

Gly Gly Gly Gly Gly Leu Ala His Gln Phe Ser Leu Pro Lys Thr Ser
          35           40           45

```

```

Ser Glu Met Ala Ala Ile Glu Lys Phe Leu Gln Phe Gln Asp Ala Val
          50           55           60

```

```

Pro Cys Lys Ile Arg Ala Lys Arg Gly Cys Ala Thr His Pro Arg Ser
65           70           75           80

```

```

Ile Ala Glu Arg Val Arg Arg Thr Arg Ile Ser Glu Arg Ile Arg Lys
          85           90           95

```

```

Leu Gln Glu Leu Val Pro Asn Met Asp Lys Gln Thr Asn Thr Ala Asp
          100           105           110

```

```

Met Leu Asp Leu Ala Val Asp Tyr Ile Lys Asp Leu Gln Lys Gln Val
          115           120           125

```

```

Lys Gly Leu Asn Asp Ser Arg Ala Asn Cys Thr Cys Ser Ala Lys His

```

130

135

140

Gln Gln Tyr Ser Gly
145

<210> 175
<211> 1164
<212> DNA
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3746 Predicted polypeptide sequence is orthologous to G3086

<400> 175
atgaacagga tgacggcgcc gcacgggggg atgccgccgc cgccgatgcc ggcgggcggg 60
gggctggcga ggtacggctc ggcgccgggg tcgctgctgg cgtcgatcgc cgactcggtg 120
atccggggcc gcggggttgg ggttgctgat cagctgcac atcatcagca tcagcatcag 180
cttcgccgc cgccgccgcc gcagcagcag cagatggtgg ggaggtactt ctccgcggag 240
tcgtcggggc tcacctcctg cgagtccagc tgccggacga cgacgacgac gtccacagcg 300
gcggcgggcc atgtcgggcg gcacccgctc gagcgcgct acggcggtc cggcgagatc 360
cacgtcgacg cctcctccgc cgccgtcccg ctcttcgcc acagcagctc ccccgccggc 420
ctcctctccc gcctcatggc tgacccgcac ggcaatggca tggccgcgac gagagggatg 480
ggcggtact ccggcgggcg cggcgacgcc ggcgcgatgg cgcacaggag gctgagctcg 540
cagtggagct tctcgcgga ggacctgcc cagatatcgg agatgggcgg cctcatcccc 600
gacatcgggg agagcatcgt caccggcgcc ggcggaaca gctccagcga tggcgccggc 660
cacggcgcg agtcctctc ctctctctcc tccaggaact tctccatgag ctctggggac 720
gacaccaact ccatcatgtt ctgcccccg agcagcagca agaaggcccg cgtcgccgcc 780
gccgcggccg gcgaccacgg cgacgacatg gtctccagct tcagcaacat cgactcccag 840
tttggttgt cgaagcagtc gtcgctggag atggccggca tggatgactt cttgcagctc 900
cagccagact ccgtcgctg caggggcccg gcaaagcgcg gctgcgagc gcacccgcgg 960
agcatcgctg agaggagag gagaacgagg attagcaaga ggctgaagaa gctgcaggat 1020
ctcgtgccga acatggacaa gcaaacgaat acatcagaca tggttgatat tgctgtaacc 1080
tacatcaagg agcttcaggg ccaagttgag aagctaaaac atgaccaagc aaactgcact 1140
tgctcaggca agcagattg ctga 1164

<210> 176
<211> 387
<212> PRT
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3746 polypeptide Orthologous to G3086

<400> 176

Met Asn Arg Met Thr Ala Pro His Gly Gly Met Pro Pro Pro Pro Met
1 5 10 15

Pro Ala Ala Gly Gly Leu Ala Arg Tyr Gly Ser Ala Pro Gly Ser Leu
20 25 30

Leu Ala Ser Ile Ala Asp Ser Val Ile Arg Gly Arg Gly Val Gly Val
35 40 45

Val Asp Gln Leu His His His Gln His Gln His Gln Leu Pro Pro Pro
50 55 60

Pro Pro Pro Gln Gln Gln Gln Met Val Gly Arg Tyr Phe Ser Ala Glu
65 70 75 80

Ser Ser Gly Leu Thr Ser Cys Glu Ser Ser Cys Arg Thr Thr Thr Thr
85 90 95

Thr Ser Thr Ala Ala Ala Ala Asp Val Gly Arg His Pro Leu Glu Arg
100 105 110

Ala Tyr Gly Gly Ser Gly Glu Ile His Val Asp Ala Ser Ser Ala Ala
115 120 125

Val Pro Leu Phe Arg His Ser Ser Ser Pro Ala Gly Leu Leu Ser Arg
130 135 140

Leu Met Ala Asp Pro His Gly Asn Gly Met Ala Ala Thr Arg Gly Met
145 150 155 160

Gly Gly Tyr Ser Gly Gly Gly Gly Asp Ala Gly Ala Met Ala His Arg
165 170 175

Arg Leu Ser Ser Gln Trp Ser Phe Ser Arg Gln Asp Leu Pro Gln Ile
180 185 190

Ser Glu Met Gly Gly Leu Ile Pro Asp Ile Gly Glu Ser Ile Val Thr
195 200 205

Gly Gly Gly Gly Asn Ser Ser Ser Asp Gly Ala Gly His Gly Ala Gln
210 215 220

Ser Ser Ser Phe Leu Ser Ser Arg Asn Phe Ser Met Ser Ser Trp Asp
225 230 235 240

Asp Thr Asn Ser Ile Met Phe Ser Pro Pro Ser Ser Ser Lys Lys Ala
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245

250

255

Arg Val Ala Ala Ala Ala Gly Asp His Gly Asp Asp Met Val Ser
260 265 270

Ser Phe Ser Asn Ile Asp Ser Gln Phe Gly Leu Ser Lys Gln Ser Ser
275 280 285

Leu Glu Met Ala Gly Met Asp Asp Phe Leu Gln Leu Gln Pro Asp Ser
290 295 300

Val Ala Cys Arg Ala Arg Ala Lys Arg Gly Cys Ala Thr His Pro Arg
305 310 315 320

Ser Ile Ala Glu Arg Glu Arg Arg Thr Arg Ile Ser Lys Arg Leu Lys
325 330 335

Lys Leu Gln Asp Leu Val Pro Asn Met Asp Lys Gln Thr Asn Thr Ser
340 345 350

Asp Met Leu Asp Ile Ala Val Thr Tyr Ile Lys Glu Leu Gln Gly Gln
355 360 365

Val Glu Lys Leu Lys His Asp Gln Ala Asn Cys Thr Cys Ser Gly Lys
370 375 380

His Asp Cys
385

<210> 177
<211> 531
<212> DNA
<213> Zea mays

<220>
<223> G3755 Predicted polypeptide sequence is orthologous to G3086

<400> 177
atgtcccaga tctcagagat ggacagcgag gaggtcggag ggagcagccc agaggctgcc 60
ggcggcggca gggggtacat ccctgggtac ccaatgggct ctgggtggga ggactcgtcg 120
gctctcttgt cagacaattt gtctggcatc aaacgcccc gggactcgtc ggagcctggc 180
cagagcggcc ttacgcacca gttagcgtg cccaagacgt cgtccgagat ggcaactatt 240
gagaaattcc tccagttcca ggacgccgtg ccttgtaaga tccgtgccaa gcggggggtgc 300
gccactcatc cacgcagcat cgctgagagg gtgaggagaa caaagatcag tgagcgaatc 360
cgaaagctgc aagaactcgt tccaaatatg gacaagcaaa ccaacacatc tgacatgctg 420
gatttggtgt tcgactacat caaggatctc cagaagcagg ttaagggtgt aaaggagagc 480

caagataatt gcacctgctc agcaagcaag aaccagcagc actcctgctg a

531

<210> 178
 <211> 176
 <212> PRT
 <213> Zea mays

<220>

<223> G3755 polypeptide Orthologous to G3086

<400> 178

Met Ser Gln Ile Ser Glu Met Asp Ser Glu Glu Val Gly Gly Ser Ser
 1 5 10 15

Pro Glu Ala Ala Gly Gly Gly Arg Gly Tyr Ile Pro Gly Tyr Pro Met
 20 25 30

Gly Ser Gly Trp Glu Asp Ser Ser Ala Leu Leu Ser Asp Asn Leu Ser
 35 40 45

Gly Ile Lys Arg Pro Arg Asp Ser Ser Glu Pro Gly Gln Ser Gly Leu
 50 55 60

Thr His Gln Phe Ser Val Pro Lys Thr Ser Ser Glu Met Ala Thr Ile
 65 70 75 80

Glu Lys Phe Leu Gln Phe Gln Asp Ala Val Pro Cys Lys Ile Arg Ala
 85 90 95

Lys Arg Gly Cys Ala Thr His Pro Arg Ser Ile Ala Glu Arg Val Arg
 100 105 110

Arg Thr Lys Ile Ser Glu Arg Ile Arg Lys Leu Gln Glu Leu Val Pro
 115 120 125

Asn Met Asp Lys Gln Thr Asn Thr Ser Asp Met Leu Asp Leu Ala Val
 130 135 140

Asp Tyr Ile Lys Asp Leu Gln Lys Gln Val Lys Val Leu Lys Glu Ser
 145 150 155 160

Gln Asp Asn Cys Thr Cys Ser Ala Ser Lys Asn Gln Gln His Ser Cys
 165 170 175

<210> 179
 <211> 711
 <212> DNA
 <213> Glycine max

<220>

<223> G3763 Predicted polypeptide sequence is orthologous to G3086

```

<400> 179
atggcaaatc ttgcagcagc attgagagat gtggcaagtt ttaggggctg tgatgtctca      60
aatggacaag ctattacatc ctctagtggg ttgcatggta ctttgaactt ctcatctagg      120
ccatcctctt gctccacccg gatgccacag attgctgaaa atggaaatga agatgtggaa      180
gcaaatgtgt ttgaaagtag aaacctgaga aatgacaata tcaacaccac taaatgttac      240
atgcctagtt tcaccactga cttctgggat ggttctgcat tcagtgcctc cagaacagct      300
agtaacagag gtgaaatctc attttccact tcaaaggcta tggatattca ggatgaagat      360
tttgataacc aaaaagttgg tttgaccac catttgagtc tgcttggtc ttccagtagg      420
atggctacaa tggagaagct ttatcaaatt caaggatctg ttccatgtaa aattcgtgcc      480
aagagagggt ttgccactca cccgagaagt attgctgaaa gggaaaggag aacacgaatt      540
agcgcaagaa tcaagaaatt gcaagacctt ttcccaaat cagacaagca aacaagcact      600
gcagatatgt tggatttggc agttgagtac attaaagact tgcagaaaca agttaagatt      660
ctcagagata ctagggcaaa ttgcacttgt acaagcaatc agaagcactg a              711

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<210> 180
<211> 236
<212> PRT
<213> Glycine max

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<220>
<223> G3763 polypeptide Orthologous to G3086

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<400> 180

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Met Ala Asn Leu Ala Ala Ala Leu Arg Asp Val Ala Ser Phe Arg Gly
1          5          10          15

Cys Asp Val Ser Asn Gly Gln Ala Ile Thr Ser Ser Ser Gly Leu His
20        25        30

Gly Thr Leu Asn Phe Ser Ser Arg Pro Ser Ser Cys Ser Thr Arg Met
35        40        45

Pro Gln Ile Ala Glu Asn Gly Asn Glu Asp Val Glu Ala Asn Cys Val
50        55        60

Glu Ser Arg Asn Leu Arg Asn Asp Asn Ile Asn Thr Thr Lys Cys Tyr
65        70        75        80

Met Pro Ser Phe Thr Thr Asp Phe Trp Asp Gly Ser Ala Phe Ser Ala
85        90        95

Ser Arg Thr Ala Ser Asn Arg Gly Glu Ile Ser Phe Ser Thr Ser Lys
100       105       110

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Ala Met Asp Ile Gln Asp Glu Asp Phe Gly Tyr Gln Lys Val Gly Leu
115 120 125

Thr His His Leu Ser Leu Pro Gly Ser Ser Ser Arg Met Ala Thr Met
130 135 140

Glu Lys Leu Tyr Gln Ile Gln Gly Ser Val Pro Cys Lys Ile Arg Ala
145 150 155 160

Lys Arg Gly Phe Ala Thr His Pro Arg Ser Ile Ala Glu Arg Glu Arg
165 170 175

Arg Thr Arg Ile Ser Ala Arg Ile Lys Lys Leu Gln Asp Leu Phe Pro
180 185 190

Lys Ser Asp Lys Gln Thr Ser Thr Ala Asp Met Leu Asp Leu Ala Val
195 200 205

Glu Tyr Ile Lys Asp Leu Gln Lys Gln Val Lys Ile Leu Arg Asp Thr
210 215 220

Arg Ala Asn Cys Thr Cys Thr Ser Asn Gln Lys His
225 230 235

<210> 181

<211> 1356

<212> DNA

<213> Glycine max

<220>

<223> G3764 Predicted polypeptide sequence is orthologous to G3086

<400> 181

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ggactattga ggtattgttc tgctccaagc tcattgctgg caagcctcat tgacaacacc	180
attcatggct gtgtcaacga ggaatcgttc acaagtgaga atcatcatca tcatcagcag	240
cagcagcagc agcattatct tccatctaca agttcagaaa tggagaccat gttatccaaa	300
ttgctaccat ccaacaatgg atggagcaat tcagaagctt tgcaagaatt tggaggcaag	360
ccctgtgaag caggaaatag gggaatctat tccacaagag ccaccacaac agaatggtta	420
ttcttatggg ggctctcagt tgatttacca atctcagcaa attcaaggcc ttgccaaatg	480
gtggactctc cagtggcttc tggcagtgct tttgatggct cttttgggtgt ggtgcactcc	540
atggcttcag aggactccat tcaatctaaa atgggtatca ggaattgctc caatctcttt	600
aggcaaaaga gttcccctgc tgcatttttc tccattgaaa atgatcttgc agcattgaga	660

MBI0058CIP.ST25.txt

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gaagtaggaa gctttaaaagc cgatgatggt tcaaattggac tagttactgc atcaactggg 720
gggttgcata gttctcatatc tttctcatct aggccatctt catgcttgaa acggttgcca 780
caaatagccg aaaatggaaa tgaaagccta gaagaaaatt gtgaccaaag tagaaaccta 840
gtaaatgaca atggtagctc aaaatgttac atacctagct tcaccaatga attatgggaa 900
agttctgcat tcaatgcccc aaaaacagag aatgaagatg aaatcatggt ttccacttca 960
aatatttttg aatctcagga agcagatttc agctttcaaa atctggggtt gactcaccat 1020
ttgagtctac ctagctcttc tactaagatg tcatccatag aaaagtttct tcagattcaa 1080
ggttctgttc cttgtaaaat tcgagccaaa agaggctttg ccactcacc cagaagtatt 1140
gcagagaggg taagaagaac aagaattagt gaaagaatca agaaactgca agaccttttt 1200
ccaaaatcag aaaagcaaac aagcacagca gatatgttag atttggcagt tgagtatatt 1260
aaggacctgc agcaaaaagt taagatactc tcagattgta aggcaaagtg caaatgtaca 1320
agtaatgaga agcattacac tagaacttgt gcttga 1356

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<210> 182
 <211> 451
 <212> PRT
 <213> Glycine max

<220>
 <223> G3764 polypeptide Orthologous to G3086

<400> 182

Met Ser Val Met Tyr Ser Pro Val Leu Asn Tyr Ser Asp Val Glu His
 1 5 10 15

Gln Leu Arg Lys Asn Gln Asp Met Asp Ser Ser Ile Gly His Pro Gln
 20 25 30

Gln His Cys His Gln Pro Asn Ser Gly Leu Leu Arg Tyr Cys Ser Ala
 35 40 45

Pro Ser Ser Leu Leu Ala Ser Leu Ile Asp Asn Thr Ile His Gly Cys
 50 55 60

Val Asn Glu Glu Ser Phe Thr Ser Glu Asn His His His His Gln Gln
 65 70 75 80

Gln Gln Gln Gln His Tyr Leu Pro Ser Thr Ser Ser Glu Met Glu Thr
 85 90 95

Met Leu Ser Lys Leu Leu Pro Ser Asn Asn Gly Trp Ser Asn Ser Glu
 100 105 110

Ala Leu Gln Glu Phe Gly Gly Lys Pro Cys Glu Ala Gly Asn Arg Gly
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115

120

125

Ile Tyr Ser Thr Arg Ala Thr Thr Thr Glu Trp Leu Phe Leu Trp Trp
130 135 140

Leu Ser Val Asp Leu Pro Ile Ser Ala Asn Ser Arg Pro Cys Gln Met
145 150 155 160

Val Asp Leu Pro Val Ala Ser Gly Ser Ala Phe Asp Gly Ser Phe Gly
165 170 175

Val Val His Ser Met Ala Ser Glu Asp Ser Ile Gln Ser Lys Met Gly
180 185 190

Ile Arg Asn Cys Ser Asn Leu Phe Arg Gln Lys Ser Ser Pro Ala Ala
195 200 205

Phe Phe Ser Ile Glu Asn Asp Leu Ala Ala Leu Arg Glu Val Gly Ser
210 215 220

Phe Lys Ala Asp Asp Val Ser Asn Gly Leu Val Thr Ala Ser Thr Gly
225 230 235 240

Gly Leu His Ser Ser His Thr Phe Ser Ser Arg Pro Ser Ser Cys Leu
245 250 255

Lys Arg Leu Pro Gln Ile Ala Glu Asn Gly Asn Glu Ser Leu Glu Glu
260 265 270

Asn Cys Asp Gln Ser Arg Asn Leu Val Asn Asp Asn Gly Ser Ser Lys
275 280 285

Cys Tyr Ile Pro Ser Phe Thr Asn Glu Leu Trp Glu Ser Ser Ala Phe
290 295 300

Asn Ala Pro Lys Thr Glu Asn Glu Asp Glu Ile Met Phe Ser Thr Ser
305 310 315 320

Asn Ile Leu Glu Ser Gln Glu Ala Asp Phe Ser Phe Gln Asn Leu Gly
325 330 335

Leu Thr His His Leu Ser Leu Pro Ser Ser Ser Thr Lys Met Ser Ser
340 345 350

Ile Glu Lys Phe Leu Gln Ile Gln Gly Ser Val Pro Cys Lys Ile Arg
355 360 365

Ala Lys Arg Gly Phe Ala Thr His Pro Arg Ser Ile Ala Glu Arg Val

370

375

380

Arg Arg Thr Arg Ile Ser Glu Arg Ile Lys Lys Leu Gln Asp Leu Phe
385 390 395 400

Pro Lys Ser Glu Lys Gln Thr Ser Thr Ala Asp Met Leu Asp Leu Ala
405 410 415

Val Glu Tyr Ile Lys Asp Leu Gln Gln Lys Val Lys Ile Leu Ser Asp
420 425 430

Cys Lys Ala Lys Cys Lys Cys Thr Ser Asn Glu Lys His Tyr Thr Arg
435 440 445

Thr Cys Ala
450

<210> 183
<211> 687
<212> DNA
<213> Glycine max

<220>
<223> G3765 Predicted polypeptide sequence is orthologous to G3086

<400> 183
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atgctatcac caacctccaa aatgggcacg gaggggtatta gggtaactag acctgaggat 180
gggagacagg gaagttgcaa tgggtgatgct cgatattatg gtcttggatt cccttatgct 240
tcttggaatg agccctcaca ccccaaaaga cagcgaagta gtaatgatga gttacttttt 300
gattctcaga atggagagcc aggaaatcaa gttcaaaggc tttcgcatca tttgagtttg 360
ccaagaacgt cgtcggagat gtttgctatg gataatttgc ttcagttctc agattctggt 420
ccttgtaaaa tcagagcaaa gagaggcttt gctactcatc ctogaagcat tgccgaaagg 480
gtgagaagaa caaggatcag tgaacgaata agaaaattgc aagagcttgt tccaaccatg 540
gacaagcaaa ctagcacagc agagatgttg gacttggtt tagactacat aaaagatctt 600
cagaaacaat tcaagactct gagcgataaa cgggctaaat gcaaagtgtat aaacatgcag 660
aagtcagaag cagatcgagt tgcttga 687

<210> 184
<211> 228
<212> PRT
<213> Glycine max

<220>
<223> G3765 polypeptide Orthologous to G3086

<400> 184

Met Lys Gly Val Gly Asn Tyr Ser Gly Val Asn Gly Asn Asp Gly Glu
1 5 10 15

Leu Ser Leu Ser Met Asn Arg Met Lys Asn His Ile Ser Phe Ser Ser
20 25 30

Ile Ser Pro Ser Ser Ser Leu Gly Met Leu Ser Pro Thr Ser Lys Met
35 40 45

Gly Thr Glu Gly Ile Arg Val Thr Arg Pro Glu Asp Gly Arg Gln Gly
50 55 60

Ser Cys Asn Gly Asp Ala Arg Tyr Tyr Gly Pro Gly Phe Pro Tyr Ala
65 70 75 80

Ser Trp Asn Glu Pro Ser His Pro Lys Arg Gln Arg Ser Ser Asn Asp
85 90 95

Glu Leu Leu Phe Asp Ser Gln Asn Gly Glu Pro Gly Asn Gln Val Gln
100 105 110

Arg Leu Ser His His Leu Ser Leu Pro Arg Thr Ser Ser Glu Met Phe
115 120 125

Ala Met Asp Asn Leu Leu Gln Phe Ser Asp Ser Val Pro Cys Lys Ile
130 135 140

Arg Ala Lys Arg Gly Phe Ala Thr His Pro Arg Ser Ile Ala Glu Arg
145 150 155 160

Val Arg Arg Thr Arg Ile Ser Glu Arg Ile Arg Lys Leu Gln Glu Leu
165 170 175

Val Pro Thr Met Asp Lys Gln Thr Ser Thr Ala Glu Met Leu Asp Leu
180 185 190

Ala Leu Asp Tyr Ile Lys Asp Leu Gln Lys Gln Phe Lys Thr Leu Ser
195 200 205

Asp Lys Arg Ala Lys Cys Lys Cys Ile Asn Met Gln Lys Ser Glu Ala
210 215 220

Asp Arg Val Ala
225

<210> 185

<211> 351
 <212> DNA
 <213> Glycine max

<220>
 <223> G3766 Predicted polypeptide sequence is orthologous to G3086

<400> 185
 atgttatcac atcacttgag ttacacaaa acttcagcag agatgattac tatggagaag 60
 ttgcttcagt tccctgattc tgttccttgt aaaatcagag caaagcgagg ctgtgctact 120
 catcctcgaa gcattgctga aaggggtgaga agaactcgga tcagtgaaag aatgaggaaa 180
 ttacaagagc ttgtcccaca catggataag caaaccaaca cagcagacat gttggacttg 240
 gctgttgaat acattaaaga tcttcagaaa caattcaaga ctctaagtga aaaaagggca 300
 aactgcaagt gtataagcat gccaaaggca gatacaaadc aaattgcttg a 351

<210> 186
 <211> 116
 <212> PRT
 <213> Glycine max

<220>
 <223> G3766 polypeptide Orthologous to G3086

<400> 186

Met Leu Ser His His Leu Ser Leu Pro Lys Thr Ser Ala Glu Met Ile
 1 5 10 15

Thr Met Glu Lys Leu Leu Gln Phe Pro Asp Ser Val Pro Cys Lys Ile
 20 25 30

Arg Ala Lys Arg Gly Cys Ala Thr His Pro Arg Ser Ile Ala Glu Arg
 35 40 45

Val Arg Arg Thr Arg Ile Ser Glu Arg Met Arg Lys Leu Gln Glu Leu
 50 55 60

Val Pro His Met Asp Lys Gln Thr Asn Thr Ala Asp Met Leu Asp Leu
 65 70 75 80

Ala Val Glu Tyr Ile Lys Asp Leu Gln Lys Gln Phe Lys Thr Leu Ser
 85 90 95

Glu Lys Arg Ala Asn Cys Lys Cys Ile Ser Met Pro Lys Ala Asp Thr
 100 105 110

Asn Gln Ile Ala
 115

<210> 187

<211> 666
<212> DNA
<213> Glycine max

<220>
<221> misc_feature
<222> (234)..(234)
<223> n is a, c, g, or t

<220>
<223> G3767 Predicted polypeptide sequence is orthologous to G3086

<400> 187
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ggggacaaag ggaatcgaga aagtagtcca gacaatgaag cttttgctga tggtaacgat 180
tttatcaccg gtttccaagt tggtcattgg gatgatgctg caatcatgtc tganaacggt 240
ggtggtctca aaagatttag agaaaacgat tcaaaacat tttctggctt aaatgctggct 300
gagactcaga atgaaacagg acagactcat gtccttttg cccatcagtt gagtttgcca 360
aatacttcag ctgaaatagc tgccattgag aagtttctgc agttttcaga ttctgttccg 420
tgcaaaatcc gtgccaaacg gggctgtgcc actcaccxaa gaagcattgc agagagggtt 480
agaagaacta aaattagtga gcgtatgagg aaacttcaag atcttgcccc aaacatggac 540
aagcaaacta acacagctga tatgttggac ttggctgtgg attacatcaa agaccttcaa 600
aagcaagttc agacgctttc agattgtcat gcaaagtgtg cgtgttcaca cgagaagcaa 660
caataa 666

<210> 188
<211> 221
<212> PRT
<213> Glycine max

<220>
<221> misc_feature
<222> (78)..(78)
<223> Xaa can be any naturally occurring amino acid

<220>
<223> G3767 polypeptide Orthologous to G3086

<400> 188

Met Gly Thr Leu Gly Ala Val Asn Asn Ser Ile Glu Asp Ala Lys Phe
1 5 10 15

Ser Ser Ser Arg Arg Leu Lys Asn Gln Pro Asn Tyr Ser Ser Ser Gly
20 25 30

Arg Met Ser Ser Asn Ala Glu Ile Gly Asp Lys Gly Asn Arg Glu Ser

35

40

45

Ser Pro Asp Asn Glu Ala Phe Ala Asp Gly Asn Asp Phe Ile Thr Gly
50 55 60

Phe Gln Val Gly His Trp Asp Asp Ala Ala Ile Met Ser Xaa Asn Val
65 70 75 80

Gly Gly Leu Lys Arg Phe Arg Glu Asn Asp Ser Lys Pro Phe Ser Gly
85 90 95

Leu Asn Ala Ala Glu Thr Gln Asn Glu Thr Gly Gln Thr His Ala Pro
100 105 110

Leu Ala His Gln Leu Ser Leu Pro Asn Thr Ser Ala Glu Ile Ala Ala
115 120 125

Ile Glu Lys Phe Leu Gln Phe Ser Asp Ser Val Pro Cys Lys Ile Arg
130 135 140

Ala Lys Arg Gly Cys Ala Thr His Pro Arg Ser Ile Ala Glu Arg Val
145 150 155 160

Arg Arg Thr Lys Ile Ser Glu Arg Met Arg Lys Leu Gln Asp Leu Val
165 170 175

Pro Asn Met Asp Lys Gln Thr Asn Thr Ala Asp Met Leu Asp Leu Ala
180 185 190

Val Asp Tyr Ile Lys Asp Leu Gln Lys Gln Val Gln Thr Leu Ser Asp
195 200 205

Cys His Ala Lys Cys Thr Cys Ser His Glu Lys Gln Gln
210 215 220

<210> 189

<211> 798

<212> DNA

<213> Glycine max

<220>

<223> G3768 Predicted polypeptide sequence is orthologous to G3086

<400> 189

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aggcatagta gctctcccgaggactat tcccaaatta acattgaaaa tgtgtatgct 120

ggtgtgagag gcatggggag tttgggagct gttaacaaca gtatcgaaga tgcgaaattt 180

tctagttcga ggaggttgaa gaatcaaccg aactattcct cgtcggggag aatgtcgtcc 240

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attgctgaaa ttggggacaa agggatataga gaaagtagtc cagacagtga agcttttgct 300
gatggtaacg attttatggc cggttaccaa gttgggcatt gggatgatac tgcaatgatg 360
tctgacaacg ttggtggtct caaaagattt agtgaagaag attcaaaacc attttctggc 420
ttaaatagcgg ttgagactca gaatgaaacg ggacagactc atgctccttt ggcccatcag 480
ttgagtttgc caaatacttc agctgaaatg gctgccattg agaagtttct gcagttttca 540
gattctgttc cgtgcaaaat ccgtgccaaa cggggctgtg ccactcacc cagaagcatt 600
gcagagaggg taagaagaac taaaattagt gagcgtatga ggaaacttca ggatcttgct 660
ccaaacatgg acaagcaaac taacacagct gatatgttgg acttggctgt ggattacatc 720
aaagaccttc aaaagcaagt tcagacactt tcagattgtc atgcaaagtg tacgtgttca 780
cacgagaagc aacaataa 798

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<210> 190

<211> 265

<212> PRT

<213> Glycine max

<220>

<223> G3768 polypeptide Orthologous to G3086

<400> 190

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Met Glu Gln Gly Ser Phe Ser Met Gly Leu Arg His Ser Gly Asn Asn
1           5           10           15

```

```

Ser Asn Leu Thr Arg His Ser Ser Ser Pro Ala Gly Leu Phe Ser Gln
          20           25           30

```

```

Ile Asn Ile Glu Asn Val Tyr Ala Gly Val Arg Gly Met Gly Ser Leu
          35           40           45

```

```

Gly Ala Val Asn Asn Ser Ile Glu Asp Ala Lys Phe Ser Ser Ser Arg
          50           55           60

```

```

Arg Leu Lys Asn Gln Pro Asn Tyr Ser Ser Ser Gly Arg Met Ser Ser
65           70           75           80

```

```

Ile Ala Glu Ile Gly Asp Lys Gly Tyr Arg Glu Ser Ser Pro Asp Ser
          85           90           95

```

```

Glu Ala Phe Ala Asp Gly Asn Asp Phe Met Ala Gly Tyr Gln Val Gly
          100          105          110

```

```

His Trp Asp Asp Thr Ala Met Met Ser Asp Asn Val Gly Gly Leu Lys
          115          120          125

```

```

Arg Phe Ser Glu Glu Asp Ser Lys Pro Phe Ser Gly Leu Asn Ala Val

```

130	135	140
Glu Thr Gln Asn Glu Thr Gly Gln Thr His Ala Pro Leu Ala His Gln		
145	150	155 160
Leu Ser Leu Pro Asn Thr Ser Ala Glu Met Ala Ala Ile Glu Lys Phe		
	165	170 175
Leu Gln Phe Ser Asp Ser Val Pro Cys Lys Ile Arg Ala Lys Arg Gly		
	180	185 190
Cys Ala Thr His Pro Arg Ser Ile Ala Glu Arg Val Arg Arg Thr Lys		
	195	200 205
Ile Ser Glu Arg Met Arg Lys Leu Gln Asp Leu Val Pro Asn Met Asp		
	210	215 220
Lys Gln Thr Asn Thr Ala Asp Met Leu Asp Leu Ala Val Asp Tyr Ile		
	225	230 235 240
Lys Asp Leu Gln Lys Gln Val Gln Thr Leu Ser Asp Cys His Ala Lys		
	245	250 255
Cys Thr Cys Ser His Glu Lys Gln Gln		
	260	265

<210> 191
 <211> 948
 <212> DNA
 <213> Glycine max

<220>
 <223> G3769 Predicted polypeptide sequence is orthologous to G3086

<400> 191	
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cgaccacctt tgccaaacca gatgaagact ggtcatggaa gtagttctaa tcttatcaga	180
catggtagct cacctgctgg attgttttca aacattaaca ttgatattac tggctatgct	240
gctgttgtaa ggggcatggg aactatggga gctgctgcta ataacaccag cgaggaagca	300
aacttttcac cagcaacaag gatgaagaat aatgcaccaa acttctcttc aggactaatg	360
tcatcaaggg ctgaagttgg aaacaagagc aatacacaga acaataatgc agaaaatgaa	420
gggtttgctg aaagccaggg caatgagttt atccctgcag gtttccccgt tgggccgtgg	480
aatgattctg caatcatgtc tgacaacgtg acaggtctga agagatttag agatgaagat	540
gtgaaacat tttctggtgg tttaaagtc cctgaaagtc agaatagaac tggaggccaa	600

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gcagccattg agaagtttct gcagctctca gattctgttc cttgcaaaat tcgtgccaaa 720
cggggctgtg ccactcaccc aagaagcatt gcagagaggg ttagaagaac taaaattagt 780
gagcgaatga ggaagctaca agatctcggt cccaacatgg ataagcaaac aaacacagct 840
gacatgttgg acttggctgt tgagtacatt aaagaccttc aaaaccaagt tcagactctt 900
tcggacaatc gggcaaagtg tacgtgttca cacaagaagc agcaataa 948

<210> 192
<211> 315
<212> PRT
<213> Glycine max

<220>
<223> G3769 polypeptide Orthologous to G3086

<400> 192

Met Asn Asn Glu Pro Leu Val Leu Gln Gln Gln Gln Gln Gln Gln Gln
1 5 10 15

Gln Gln Gln Gln Ser Asn Asn Met Tyr Asn Tyr Gly Ser Ser Gly Thr
20 25 30

Gln Asn Phe Tyr Gln Ser Thr Gly Arg Pro Pro Leu Pro Asn Gln Met
35 40 45

Lys Thr Gly His Gly Ser Ser Ser Asn Leu Ile Arg His Gly Ser Ser
50 55 60

Pro Ala Gly Leu Phe Ser Asn Ile Asn Ile Asp Ile Thr Gly Tyr Ala
65 70 75 80

Ala Val Val Arg Gly Met Gly Thr Met Gly Ala Ala Ala Asn Asn Thr
85 90 95

Ser Glu Glu Ala Asn Phe Ser Pro Ala Thr Arg Met Lys Asn Asn Ala
100 105 110

Pro Asn Phe Ser Ser Gly Leu Met Ser Ser Arg Ala Glu Val Gly Asn
115 120 125

Lys Ser Asn Thr Gln Asn Asn Asn Ala Glu Asn Glu Gly Phe Ala Glu
130 135 140

Ser Gln Gly Asn Glu Phe Ile Pro Ala Gly Phe Pro Val Gly Pro Trp
145 150 155 160

Asn Asp Ser Ala Ile Met Ser Asp Asn Val Thr Gly Leu Lys Arg Phe
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175

Arg Asp Glu Asp Val Lys Pro Phe Ser Gly Gly Leu Asn Ala Pro Glu
 180 185 190

Ser Gln Asn Glu Thr Gly Gly Gln Gln Pro Ser Ser Ser Ala Leu Ala
 195 200 205

His Gln Leu Ser Leu Pro Asn Thr Ser Ala Glu Met Ala Ala Ile Glu
 210 215 220

Lys Phe Leu Gln Leu Ser Asp Ser Val Pro Cys Lys Ile Arg Ala Lys
 225 230 235 240

Arg Gly Cys Ala Thr His Pro Arg Ser Ile Ala Glu Arg Val Arg Arg
 245 250 255

Thr Lys Ile Ser Glu Arg Met Arg Lys Leu Gln Asp Leu Val Pro Asn
 260 265 270

Met Asp Lys Gln Thr Asn Thr Ala Asp Met Leu Asp Leu Ala Val Glu
 275 280 285

Tyr Ile Lys Asp Leu Gln Asn Gln Val Gln Thr Leu Ser Asp Asn Arg
 290 295 300

Ala Lys Cys Thr Cys Ser His Lys Lys Gln Gln
 305 310 315

<210> 193
 <211> 474
 <212> DNA
 <213> Glycine max

<220>
 <223> G3771 Predicted polypeptide sequence is orthologous to G3086

<400> 193
 atgcaaccca catccggcgg cggcgggctg gcaaggttcc gttcagctcc ggcgagctgg 60
 ttagaatcag ttctgttgaa ggaagaggaa gaagaagaag accccttaag cttcactcaa 120
 ctgctttcca ctatcgatga tgctccctct cattctcaac accaactcta tgggtgcccgt 180
 ctctcaaaca aggataaaac acctgaaatc ttcatgttag aagattccgt tccttgacga 240
 gtgaggggcta agcgtggctg tgctactcat cccaggagta ttgctgaaag ggttcgcagg 300
 actcgtatca gtgaccgcat cagaaagctg caagaacttg tgccaaacat ggataagcaa 360
 acaaatactg cagatatgtt agatgaggct gtagcgtatg tcaagtttct acaaaagcaa 420
 attgaggaac tgtcagagca ccaacggagg tgtaaattgcg tggttcaaga gtaa 474

<210> 194
 <211> 157
 <212> PRT
 <213> Glycine max

<220>
 <223> G3771 polypeptide Orthologous to G3086

<400> 194

Met Gln Pro Thr Ser Gly Gly Gly Gly Leu Ala Arg Phe Arg Ser Ala
 1 5 10 15

Pro Ala Ser Trp Leu Glu Ser Val Leu Leu Lys Glu Glu Glu Glu Glu
 20 25 30

Glu Asp Pro Leu Ser Phe Thr Gln Leu Leu Ser Thr Ile Asp Asp Ala
 35 40 45

Pro Ser His Ser Gln His Gln Leu Tyr Gly Ala Ala Leu Ser Asn Lys
 50 55 60

Asp Lys Thr Pro Glu Ile Phe Met Leu Glu Asp Ser Val Pro Cys Arg
 65 70 75 80

Val Arg Ala Lys Arg Gly Cys Ala Thr His Pro Arg Ser Ile Ala Glu
 85 90 95

Arg Val Arg Arg Thr Arg Ile Ser Asp Arg Ile Arg Lys Leu Gln Glu
 100 105 110

Leu Val Pro Asn Met Asp Lys Gln Thr Asn Thr Ala Asp Met Leu Asp
 115 120 125

Glu Ala Val Ala Tyr Val Lys Phe Leu Gln Lys Gln Ile Glu Glu Leu
 130 135 140

Ser Glu His Gln Arg Arg Cys Lys Cys Val Val Gln Glu
 145 150 155

<210> 195
 <211> 861
 <212> DNA
 <213> Glycine max

<220>
 <223> G3772 Predicted polypeptide sequence is orthologous to G3086

<400> 195

atgtaaccct cttcctcttc ctctctctcc tcttctcttc agtccatgac ccaagctggc 60
 ctcaactcgt acggttccgc ccccggttct cttctcacca gcacgggttg ttctttattg 120

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gtggatcccg tcccagttccc tactttttccg gagagtcttc tgagtctccc tgcaaagagc 180
aaagatcttt ccacaaccac ccccccctct tcgtcttctc cttgctccgc cagaaaagct 240
ctctcgacgg cttcctttcc catctctcca aacaccatgg ggtgggtttc aaccatcacc 300
cccggtggtt tatcaaattc aaattcaaat tcaaattggt ctctcttgaa gtctcaactc 360
agcttcaccc acgaatctct ttccaacact gttaatgttg atccctccag caccaccttc 420
ggaatggatc cctgggacaa caattccatc gccttttctg caacttcaac caagcgctcc 480
aaaaccaaca ccaatgatcc tgacatttta cattccctga attcggcctt ggaatcacag 540
ttcaatcttc cacatacaag tctggaaatg tcaaccgtgg acaagctatt gcacattcct 600
gaagattctg tcccttgtaa aatccgtgct aagcgaggtt gtgctactca tccccgtagc 660
attgccgagc gggagagaag aacaaggatc agtggcaagc tcaagaaatt acaggacctt 720
gtaccaataa tggataagca aacaagctat gcagacatgc tcgatttggc cgttcaacac 780
attaaaggtc ttcaaactca gggtcagaag cttcacaag aaatggagaa ttgcacttgc 840
ggatgcaaac aaagcaaata a 861

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<210> 196
 <211> 286
 <212> PRT
 <213> Glycine max

<220>
 <223> G3772 polypeptide Orthologous to G3086

<400> 196

Met Tyr Pro Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Gln Ser Met
 1 5 10 15

Thr Gln Ala Gly Leu Thr Arg Tyr Gly Ser Ala Pro Gly Ser Leu Leu
 20 25 30

Thr Ser Thr Val Asp Ser Leu Leu Val Asp Pro Val Pro Val Pro Thr
 35 40 45

Phe Pro Glu Ser Leu Leu Ser Leu Pro Ala Lys Ser Lys Asp Leu Ser
 50 55 60

Thr Thr Thr Pro Pro Pro Ser Leu Pro Pro Cys Ser Ala Arg Lys Ala
 65 70 75 80

Leu Ser Thr Ala Ser Phe Pro Ile Ser Pro Asn Thr Met Gly Trp Val
 85 90 95

Ser Thr Ile Thr Pro Gly Gly Leu Ser Asn Ser Asn Ser Asn Ser Asn
 100 105 110

MBI0058CIP.ST25.txt

Cys Ser Leu Leu Lys Ser Gln Leu Ser Phe Thr His Glu Ser Leu Ser
115 120 125

Asn Thr Val Asn Val Asp Pro Ser Ser Thr Thr Phe Gly Met Asp Pro
130 135 140

Trp Asp Asn Asn Ser Ile Ala Phe Ser Ala Thr Ser Thr Lys Arg Ser
145 150 155 160

Lys Thr Asn Thr Asn Asp Pro Asp Ile Leu His Ser Leu Asn Ser Ala
165 170 175

Leu Glu Ser Gln Phe Asn Leu Pro His Thr Ser Leu Glu Met Ser Thr
180 185 190

Val Asp Lys Leu Leu His Ile Pro Glu Asp Ser Val Pro Cys Lys Ile
195 200 205

Arg Ala Lys Arg Gly Cys Ala Thr His Pro Arg Ser Ile Ala Glu Arg
210 215 220

Glu Arg Arg Thr Arg Ile Ser Gly Lys Leu Lys Lys Leu Gln Asp Leu
225 230 235 240

Val Pro Asn Met Asp Lys Gln Thr Ser Tyr Ala Asp Met Leu Asp Leu
245 250 255

Ala Val Gln His Ile Lys Gly Leu Gln Thr Gln Val Gln Lys Leu His
260 265 270

Lys Glu Met Glu Asn Cys Thr Cys Gly Cys Lys Gln Ser Lys
275 280 285

<210> 197

<211> 1656

<212> DNA

<213> Pinus taeda

<220>

<223> G3782 Predicted polypeptide sequence is orthologous to G3086

<400> 197

atgtcatatg tcaaaatgct aaactctcga gctcagccca ttagcactgg tttaagcatt 60

ccatctctga gtgttgga tactgatgta aatggaatcc aaatatcggt ctcccagtac 120

cccatggact cagagaagat gcctcagatg cagcaacaga caaataatgt agactttatg 180

gacctcgatt ataagcccc tctttgcaat gtttcccaag cagatggagt aatggcatta 240

acagaaagag gttcgtccaa caattttcag ggaccaacag gattgatgcg ctaccattcg 300

MBI0058CIP.ST25.txt

gcgcccagct cttttttttc aagtctagga gaagaggaaa ataataacat tatatcagag 360
tattttctctg gtaattcttc gaatccactg caatcaaata ccaaaccact gcagcaaaat 420
caacctagta tattgagttt tcatctcagg gaaaatgaac cagcaaagca tcttggcgaa 480
cgcaatgaaa tatctgaaaa agaaatgcac gccagctccc ttcctcaaa agaagtgcag 540
ggaaatgttt ctagagaaga tctaggcaag caccatcctc ttgatgcaat ccttgagaat 600
gtaccggatg tatcccaaga cagttttggc acctctcaaa tgtcattgat gagccaagtt 660
caagtttctg aaccaagtgg acaacacatc gattcatcct accaaatgaa ttcagtttgc 720
tgcgataccc ttgatcagtc aggaggaagg atgggcaatg catactcctc aacatccaag 780
aatacactta ttcgacatag tagctcccca gctgggctac tctctgaact agttgctgaa 840
ggccgaggta cttttgaaag tggtttcatg gagggaacag tcagaaatag tattggtgtg 900
ggaaactcat gtggggatat cattatacca aatagagttc aaagacaaat gaaccgtttg 960
cagcagaata gttctcctgg actattatcc caactatctg tggatatgag tgtaccagaa 1020
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caagatgctg ttccatgcaa ggtccgggca aaaagaggct gtgcaacgca cccacggagc 1440
attgctgaaa gggttcgaag aacacgaatc agtgaaagaa tgagaaaact gcaggaactt 1500
gtgccaaaca gtgacaagca aacagtaaatt attgccgaca tgtagatga ggccgttgaa 1560
tatgtcaagt ctcttcagaa gcaggtccag gaacttgagg aaaatcgagc caagtgtacc 1620
tgcacacata atccggattg tgcatacaaa acataa 1656

<210> 198
<211> 551
<212> PRT
<213> Pinus taeda

<220>
<223> G3782 polypeptide Orthologous to G3086

<400> 198

Met Ser Tyr Val Lys Met Leu Asn Ser Arg Ala Gln Pro Ile Ser Thr
1 5 10 15

Gly Leu Ser Ile Pro Ser Leu Ser Val Gly His Thr Asp Val Asn Gly
20 25 30

MBI0058CIP.ST25.txt

Ile Gln Ile Ser Phe Ser Gln Tyr Pro Met Asp Ser Glu Lys Met Pro
35 40 45

Gln Met Gln Gln Gln Thr Asn Asn Val Asp Phe Met Asp Leu Asp Tyr
50 55 60

Lys Pro Pro Leu Cys Asn Val Ser Gln Ala Asp Gly Val Met Ala Leu
65 70 75 80

Thr Glu Arg Gly Ser Ser Asn Asn Phe Gln Gly Pro Thr Gly Leu Met
85 90 95

Arg Tyr His Ser Ala Pro Ser Ser Phe Phe Ser Ser Leu Gly Glu Glu
100 105 110

Glu Asn Asn Asn Ile Ile Ser Glu Tyr Phe Ser Gly Asn Ser Ser Asn
115 120 125

Pro Leu Gln Ser Asn Thr Lys Pro Leu Gln Gln Asn Gln Pro Ser Ile
130 135 140

Leu Ser Phe His Leu Arg Glu Asn Glu Pro Ala Lys His Leu Gly Glu
145 150 155 160

Arg Asn Glu Ile Ser Glu Lys Glu Met His Ala Ser Ser Leu Pro Ser
165 170 175

Lys Glu Val Gln Gly Asn Val Ser Arg Glu Asp Leu Gly Lys His His
180 185 190

Pro Leu Asp Ala Ile Leu Glu Asn Val Pro Asp Val Ser Gln Asp Ser
195 200 205

Phe Gly Thr Ser Gln Met Ser Leu Met Ser Gln Val Gln Val Ser Glu
210 215 220

Pro Ser Gly Gln His Ile Asp Ser Ser Tyr Gln Met Asn Ser Val Cys
225 230 235 240

Cys Asp Thr Leu Asp Gln Ser Gly Gly Arg Met Gly Asn Ala Tyr Ser
245 250 255

Ser Thr Ser Lys Asn Thr Leu Ile Arg His Ser Ser Ser Pro Ala Gly
260 265 270

Leu Leu Ser Glu Leu Val Ala Glu Gly Arg Gly Thr Phe Glu Ser Gly
275 280 285

MBI0058CIP.ST25.txt

Phe Met Glu Gly Thr Val Arg Asn Ser Ile Gly Val Gly Asn Ser Cys
 290 295 300

 Gly Asp Ile Ile Ile Pro Asn Arg Val Gln Arg Gln Met Asn Arg Leu
 305 310 315 320

 Gln Gln Asn Ser Ser Pro Gly Leu Leu Ser Gln Leu Ser Val Asp Met
 325 330 335

 Ser Val Pro Glu Met Val Asp Arg Leu Asn Met Ala Met Val Gly Ser
 340 345 350

 Ser Ala Glu Asn Gln Ala Gly Ser Ser Ser Asp Asp Ser Ser Leu Gly
 355 360 365

 Ser Gly Asn Ala Gly Gln Gly Tyr Ile Ser Asn Phe Ser Val Lys Ser
 370 375 380

 Trp Asp Asp Glu Ala Met Thr Pro Gly Asn Phe Ala Gly Met Gln Asn
 385 390 395 400

 Gly Ala Asn Phe Thr Ala Arg Lys Arg Ala Lys Glu Leu Asp Met Lys
 405 410 415

 Leu Met Gln Gly Leu Asn Asn Ser Asp His Gln Lys Val Glu Gly Gly
 420 425 430

 Ile Arg Gly Ala Ser Ala Leu Thr Asn His Pro Tyr Asn Leu Pro Arg
 435 440 445

 Ser Thr Ser Ser Glu Leu Ala Met Glu Glu Phe Leu Gln Asp Ala Val
 450 455 460

 Pro Cys Lys Val Arg Ala Lys Arg Gly Cys Ala Thr His Pro Arg Ser
 465 470 475 480

 Ile Ala Glu Arg Val Arg Arg Thr Arg Ile Ser Glu Arg Met Arg Lys
 485 490 495

 Leu Gln Glu Leu Val Pro Asn Ser Asp Lys Gln Thr Val Asn Ile Ala
 500 505 510

 Asp Met Leu Asp Glu Ala Val Glu Tyr Val Lys Ser Leu Gln Lys Gln
 515 520 525

 Val Gln Glu Leu Ala Glu Asn Arg Ala Lys Cys Thr Cys Thr His Asn
 530 535 540

Pro Asp Cys Ala Tyr Lys Thr
545 550

<210> 199
<211> 918
<212> DNA
<213> Zea mays

<220>
<223> G3794 Predicted polypeptide sequence is orthologous to G1792

<400> 199
attacttgtg cacttggtg cagtgcctgc agtataatca agttagggtt taaaagaacc 60
tcgaccgcga tcgtatatag atccagatta tcattagtta ttagaccact gtgatatcga 120
tggacgacgg cggcgagcca accaagtacc gcggcgtgcg gcgccggccg tcggggaagt 180
tcgccgccga gatccgcgac tccagccggc agagcgtgcg catgtggctg ggcaccttcg 240
acacggccga ggaggccgca agggcgtacg accgcgcggc ctacgccatg cgcggccaaa 300
tcgccgtgct caacttcccc gccgaggcgc gcaactacgt gcgcggcggg tcgtcgtcgt 360
cccgccagca gcagcaggga ggaggaggag gaggaggaag tggcggcggc gccggtcagc 420
aggtgatcga gctggagtgc ctggacgatc aggtgctgca ggagatgctc aagggcggcg 480
acgggaaaaa atagttgtta gcgtatctga tcacagggtgc acgtgttgaa actgattatg 540
accagycgat cgatcccatc ttgtgcatgc ggccctgcaa agttgctggg tcttctcatc 600
gacctatata tatatgcttc tcgatccata tatatatcat aaatgcatgc aggggtgatg 660
catgtaccaa gtttgaatt ataatgctct tgggtgctgaa ttgaagtata ctagtatata 720
tagtgtgatc catgtattga aaaggttgtt ttgcttaatc gcgtcatgat tgcacacgtg 780
cttgtttctg cttaaacaac ccatatatat agccggctct ggcccttctg aagtctgcaa 840
tccttatata tcgttggtta ttcatgcatg agttctatgt aactgcaatt tagataaatt 900
gtagctaata taatagtc 918

<210> 200
<211> 124
<212> PRT
<213> Zea mays

<220>
<223> G3794 polypeptide Orthologous to G1792

<400> 200

Met Asp Asp Gly Gly Glu Pro Thr Lys Tyr Arg Gly Val Arg Arg Arg
1 5 10 15

Pro Ser Gly Lys Phe Ala Ala Glu Ile Arg Asp Ser Ser Arg Gln Ser
20 25 30

MBI0058CIP.ST25.txt

Val Arg Met Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Arg
35 40 45

Ala Tyr Asp Arg Ala Ala Tyr Ala Met Arg Gly Gln Ile Ala Val Leu
50 55 60

Asn Phe Pro Ala Glu Ala Arg Asn Tyr Val Arg Gly Gly Ser Ser Ser
65 70 75 80

Ser Arg Gln Gln Gln Gln Gly Gly Gly Gly Gly Gly Gly Ser Gly Gly
85 90 95

Gly Ala Gly Gln Gln Val Ile Glu Leu Glu Cys Leu Asp Asp Gln Val
100 105 110

Leu Gln Glu Met Leu Lys Gly Gly Asp Gly Lys Lys
115 120

<210> 201
<211> 760
<212> DNA
<213> Capsicum annuum

<220>
<223> G3795 Predicted polypeptide sequence is orthologous to G1274

<400> 201
aaataatccc agtgcaaaca tgcttgatgg gagttttaga tcattggact cacctgacag 60
tgatgatttc tcaaaccacc taattaactt tgagctttct gatattctcg aaatagataa 120
ttggcccatt caacaagatc cgacactcat accccagtac tcaaattatg cagcaaacca 180
agtggttaac accagcagtt accaggaaga acctagcaac aacattggaa gcagcagcag 240
caagaggaaa gaagtaaagg acaagggtgc ttccagaacg ctatcacaga ttgaaatact 300
agacgatggc tataagtgga gaaagtatgg aaagaagatg gtgaaaaata gtcccaaccc 360
gaggaattac tatagggtgt ccgtagaagg ttgtccagtg aagaagagag ttgaacgaga 420
caaagaggac tctcggtatg tgataaccac ctacgagggt gtccacaacc atcaaggtct 480
atccccattc tgattcctgt aacagagctc gagtttgaaa gttactatga ctcttgcacg 540
gtagctagct aaatcagggt tctactgcca gtaaattgaa tcctgacagc ttggcgagtt 600
cataaccaaa cattgtgggg tggtcagacg gaggcacga tctgtaactt aaaagtaatc 660
gttagaacat ttcgtgccct tcagttggca tgtagtctta tcctgcttcc tacatgattt 720
atatatccta cagcactatc aactaaaaaa aaaaaaaaaa 760

<210> 202
<211> 157
<212> PRT

<213> Capsicum annuum

<220>

<223> G3795 polypeptide Orthologous to G1274

<400> 202

Met Leu Asp Gly Ser Phe Arg Ser Leu Asp Ser Pro Asp Ser Asp Asp
1 5 10 15

Phe Ser Asn His Leu Ile Asn Phe Glu Leu Ser Asp Ile Leu Glu Ile
20 25 30

Asp Asn Trp Pro Ile Gln Gln Asp Pro Thr Leu Ile Pro Gln Tyr Ser
35 40 45

Asn Tyr Ala Ala Asn Gln Val Val Asn Thr Ser Ser Tyr Gln Glu Glu
50 55 60

Pro Ser Asn Asn Ile Gly Ser Ser Ser Ser Lys Arg Lys Glu Val Lys
65 70 75 80

Asp Lys Val Ala Phe Arg Thr Leu Ser Gln Ile Glu Ile Leu Asp Asp
85 90 95

Gly Tyr Lys Trp Arg Lys Tyr Gly Lys Lys Met Val Lys Asn Ser Pro
100 105 110

Asn Pro Arg Asn Tyr Tyr Arg Cys Ser Val Glu Gly Cys Pro Val Lys
115 120 125

Lys Arg Val Glu Arg Asp Lys Glu Asp Ser Arg Tyr Val Ile Thr Thr
130 135 140

Tyr Glu Gly Val His Asn His Gln Gly Leu Ser Pro Phe
145 150 155

<210> 203

<211> 712

<212> DNA

<213> Lactuca sativa

<220>

<223> G3797 Predicted polypeptide sequence is orthologous to G1274

<400> 203

ggcataccaa aatgaattat tatgatcatc aaatgtctaa agcctacagt tacagatcag	60
tagactcgcc tgacatggac tatgatgttc caaaccagca aacttatgag tttgttgaga	120
gctttctcag ctttgatgat tggataactg aagataaagc atccactgtt cctgagtatc	180
aagatcatatc tcctgtttac ccttctgcca ccattgaaga tgggtggtctg tcgatcggaa	240

MBI0058CIP.ST25.txt

gtagcagcag caacagccat cttcatgatg gaagtagaag cagggccaca ggatttgggc 300
aggctcaaaa tggcaaaaaa gagaaagtcg ctttcaaaac aaaatcccaa gttgagatcc 360
tagatgacgg ttttaagtgg aggaaatatg gcaaaaagat ggtaaaaaac agtccaaacc 420
caaggaatta ttatcgttgt tcagcagcag gatgttcggt gaaaaagaga gttgaaaggg 480
atgtagagga tgcacgatat gtaatcacia cctacgaggg tattcacaac caccaacgcc 540
cttctaacta ctgatagctt gtactacgat ttgttaatgt atgctaaaga atagttgttt 600
ttctaagctt actccatcac tagcttattg aaaagaaagt tgtagttcgg ttacttattt 660
tcttcaaccg accaagggtta tgaatcgttt tagaatataa ttgtttttta ct 712

<210> 204

<211> 180

<212> PRT

<213> Lactuca sativa

<220>

<223> G3797 polypeptide Orthologous to G1274

<400> 204

Met Asn Tyr Tyr Asp His Gln Met Ser Lys Ala Tyr Ser Tyr Arg Ser
1 5 10 15

Val Asp Ser Pro Asp Met Asp Tyr Asp Val Pro Asn Gln Gln Thr Tyr
20 25 30

Glu Phe Val Glu Ser Phe Leu Ser Phe Asp Asp Trp Ile Thr Glu Asp
35 40 45

Lys Ala Ser Thr Val Pro Glu Tyr Gln Asp His Thr Pro Val Tyr Pro
50 55 60

Ser Ala Thr Ile Glu Asp Gly Gly Leu Ser Ile Gly Ser Ser Ser Ser
65 70 75 80

Asn Ser His Leu His Asp Gly Ser Arg Ser Arg Ala Thr Gly Phe Gly
85 90 95

Gln Ala Gln Asn Gly Lys Lys Glu Lys Val Ala Phe Lys Thr Lys Ser
100 105 110

Gln Val Glu Ile Leu Asp Asp Gly Phe Lys Trp Arg Lys Tyr Gly Lys
115 120 125

Lys Met Val Lys Asn Ser Pro Asn Pro Arg Asn Tyr Tyr Arg Cys Ser
130 135 140

Ala Ala Gly Cys Ser Val Lys Lys Arg Val Glu Arg Asp Val Glu Asp

145

150

155

160

Ala Arg Tyr Val Ile Thr Thr Tyr Glu Gly Ile His Asn His Gln Arg
165 170 175

Pro Ser Asn Tyr
180

<210> 205
<211> 866
<212> DNA
<213> Sorghum bicolor

<220>
<223> G3802 Predicted polypeptide sequence is orthologous to G1274

<400> 205
gcacgaggct gatacacaag caaggcggct agctacagct agctgggtgcg tgcagtgcac 60
gcaaatggcg gcttccctgg gactgaaccc tgaagctctc ttcgcttcat actcgtctgc 120
ctactcctcc tctcgcgctg tcgtgtccga ctacgcggcg agcttcccgg cggccgtcga 180
ctccgccacg gccttctccg cggagctcga tgaccttcac cacttcgact actcaccggc 240
gccgatcttc acagctgtcg gagccggggc tggcggcgat cgcaacgaga agatgatgat 300
gtgggtgtgag ggcgggtggtg atgaaaagag actcagaagc agtggaagga tcgggttcag 360
aacgagatca gaggtggaga tcttggacga tggattcaaa tggaggaagt atgggaagaa 420
ggctgtcaag aacagcccaa atccaaggaa ctactaccgc tgctcgtcgg agggctgcgg 480
cgtgaagaag cgggtggaga gggaccgcga cgacccccgc tacgtcatca ccacctacga 540
cggcgtccac aaccacgcca gtcccggagc cgccgccatc atccagtagc gcggcggcgg 600
cggcaatagc ggcttctaca gcccgcgca cagtggctcg ccgtcggctg cctcactctc 660
gggctccttc gtcttctgac ttttccgggc cttgaccttg acccagagtg atttaccttt 720
acccagtcg taggatgaga agagtgttca gagagatcag ttcagcggcc ggctaaattc 780
cgacctgctt gtacattttt acacacttgt gcagtacaag taataatatt taagctagaa 840
gcagtgtact ctactttatt tacctc 866

<210> 206
<211> 206
<212> PRT
<213> Sorghum bicolor

<220>
<223> G3802 polypeptide Orthologous to G1274

<400> 206

Met Gln Met Ala Ala Ser Leu Gly Leu Asn Pro Glu Ala Leu Phe Ala
1 5 10 15

MBI0058CIP.ST25.txt

Ser Tyr Ser Ser Ala Tyr Ser Ser Ser Ser Pro Phe Val Ser Asp Tyr
20 25 30

Ala Ala Ser Phe Pro Ala Ala Val Asp Ser Ala Thr Ala Phe Ser Ala
35 40 45

Glu Leu Asp Asp Leu His His Phe Asp Tyr Ser Pro Ala Pro Ile Phe
50 55 60

Thr Ala Val Gly Ala Gly Ala Gly Gly Asp Arg Asn Glu Lys Met Met
65 70 75 80

Met Trp Cys Glu Gly Gly Gly Asp Glu Lys Arg Leu Arg Ser Ser Gly
85 90 95

Arg Ile Gly Phe Arg Thr Arg Ser Glu Val Glu Ile Leu Asp Asp Gly
100 105 110

Phe Lys Trp Arg Lys Tyr Gly Lys Lys Ala Val Lys Asn Ser Pro Asn
115 120 125

Pro Arg Asn Tyr Tyr Arg Cys Ser Ser Glu Gly Cys Gly Val Lys Lys
130 135 140

Arg Val Glu Arg Asp Arg Asp Asp Pro Arg Tyr Val Ile Thr Thr Tyr
145 150 155 160

Asp Gly Val His Asn His Ala Ser Pro Gly Ala Ala Ala Ile Ile Gln
165 170 175

Tyr Gly Gly Gly Gly Gly Asn Ser Gly Phe Tyr Ser Pro Pro His Ser
180 185 190

Gly Ser Pro Ser Ala Ala Ser Tyr Ser Gly Ser Phe Val Phe
195 200 205

<210> 207

<211> 643

<212> DNA

<213> Glycine max

<220>

<223> G3803 Predicted polypeptide sequence is orthologous to G1274

<400> 207

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aatcctaaac cttatgataa ccgtcactct gccgtagtaa acacggaatc tccttcctcc 120

gagttcatgc tatctgatta tctcgtgttg gaagatgctg tcgataatca agagtcttg 180

MBI0058CIP.ST25.txt

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tcacaaagca ctgaaactga atcatcggag aaaggaaact ccagcgatgt cagtcatggg      240
tttggtgatg caaccttcag caacaccaac atgcatataa agtgcgaaaa taatgggata      300
aagcgaaaga aggaagaagt gagtcaaatt atcacgttta gaaccagatc gcagcttgag      360
gttatggatg atggatataa atggaggaaa tacggaaaga agacagtga gaacaatccc      420
aaccgaagga actactacaa gtgttcaggt gaaggatgca atgtgaagaa aaggggtggaa      480
agagacaggg atgactcgaa ctatgtttta acaacgtacg acggtgtcca caatcatgag      540
agcccgtcga ctgcctacta cagccaaatt cccttggtgc attctaacca tgattggccc      600
cagctgcacc cttctgcaaa ctcatgatcc tcttcaatac agt                        643

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<210> 208
 <211> 196
 <212> PRT
 <213> Glycine max

<220>
 <223> G3803 polypeptide Orthologous to G1274

<400> 208

Met Asp Tyr Tyr Phe Gly Asn Pro Asn Pro Lys Pro Tyr Asp Asn Arg
 1 5 10 15

His Ser Ala Val Val Asn Thr Glu Ser Pro Ser Ser Glu Phe Met Leu
 20 25 30

Ser Asp Tyr Leu Val Leu Glu Asp Ala Val Asp Asn Gln Glu Ser Trp
 35 40 45

Ser Gln Ser Thr Glu Thr Glu Ser Ser Glu Lys Gly Asn Ser Ser Asp
 50 55 60

Val Ser His Gly Phe Gly Asp Ala Thr Phe Ser Asn Thr Asn Met His
 65 70 75 80

Ile Lys Cys Glu Asn Asn Gly Ile Lys Arg Lys Lys Glu Glu Val Ser
 85 90 95

Gln Met Ile Thr Phe Arg Thr Arg Ser Gln Leu Glu Val Met Asp Asp
 100 105 110

Gly Tyr Lys Trp Arg Lys Tyr Gly Lys Lys Thr Val Lys Asn Asn Pro
 115 120 125

Asn Pro Arg Asn Tyr Tyr Lys Cys Ser Gly Glu Gly Cys Asn Val Lys
 130 135 140

Lys Arg Val Glu Arg Asp Arg Asp Asp Ser Asn Tyr Val Leu Thr Thr

145 150 155 160

Tyr Asp Gly Val His Asn His Glu Ser Pro Ser Thr Ala Tyr Tyr Ser
165 170 175

Gln Ile Pro Leu Val His Ser Asn His Asp Trp Pro Gln Leu His Pro
180 185 190

Ser Ala Asn Ser
195

<210> 209
<211> 823
<212> DNA
<213> Zea mays

<220>
<221> misc_feature
<222> (9)..(9)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (802)..(802)
<223> n is a, c, g, or t

<220>
<223> G3804 Predicted polypeptide sequence is orthologous to G1274

<400> 209
ccggccgng atattcaggc aggcgcattg actggtacgc atacaactac aagcaaggcg 60
gctagctaca gcggttagtg cgcgctggt gcaggcgag ctagctagtg cgtgcaatgg 120
cgacttcgct gggactgaac cctgaagatc tcttcacttc gtactcgtct tcctactact 180
cctcgccgcc gttcatgtcc gactacgcgg cgagcttcac gccggcgggc ggggactcca 240
cggccttctc ctccgagctc gacaaccttc accacttcga ctactcaccg gcgccgatcg 300
tactgctgc cgagccggg gctgggggcg gcgatcgaa cgagaagatg atgtggtgtc 360
agggtggtgg tgacgagaga agactcagaa gcaacggaag gatcgggttc agaaccgaggt 420
cacaggtgga gatcttgac gacggattca agtggaggaa gtacgggaag aaggccgtca 480
agaacagccc aaatccaagg aactactacc gctgctcgtc ggagggctgc ggcgtgaaga 540
agcggtgga gagggaccgc gacgacccc gctacgtcat caccacctac gacggcgtcc 600
acaaccacgc cagccccgca gccgctgcta tcatcgtccc gtacggcaac ggcggcggca 660
atagcggctt ctacagcccg ccgcacagcg gctccccgtc ggccacctcc tactcgggct 720
ccctagtctt ctgacttttc cgggccttga cccatagtta cctttacacc ccagtcgctg 780
gatgagaaga atcttcagcg gncggctaaa cagtctcaac tgc 823

<210> 210
 <211> 205
 <212> PRT
 <213> Zea mays

<220>
 <223> G3804 polypeptide Orthologous to G1274

<400> 210

Met Ala Thr Ser Leu Gly Leu Asn Pro Glu Asp Leu Phe Thr Ser Tyr
 1 5 10 15

Ser Ser Ser Tyr Tyr Ser Ser Pro Pro Phe Met Ser Asp Tyr Ala Ala
 20 25 30

Ser Phe Thr Pro Ala Gly Gly Asp Ser Thr Ala Phe Ser Ser Glu Leu
 35 40 45

Asp Asn Leu His His Phe Asp Tyr Ser Pro Ala Pro Ile Val Thr Ala
 50 55 60

Ala Gly Ala Gly Ala Gly Gly Gly Asp Arg Asn Glu Lys Met Met Trp
 65 70 75 80

Cys Gln Gly Gly Gly Asp Glu Arg Arg Leu Arg Ser Asn Gly Arg Ile
 85 90 95

Gly Phe Arg Thr Arg Ser Gln Val Glu Ile Leu Asp Asp Gly Phe Lys
 100 105 110

Trp Arg Lys Tyr Gly Lys Lys Ala Val Lys Asn Ser Pro Asn Pro Arg
 115 120 125

Asn Tyr Tyr Arg Cys Ser Ser Glu Gly Cys Gly Val Lys Lys Arg Val
 130 135 140

Glu Arg Asp Arg Asp Asp Pro Arg Tyr Val Ile Thr Thr Tyr Asp Gly
 145 150 155 160

Val His Asn His Ala Ser Pro Ala Ala Ala Ala Ile Ile Val Pro Tyr
 165 170 175

Gly Asn Gly Gly Gly Asn Ser Gly Phe Tyr Ser Pro Pro His Ser Gly
 180 185 190

Ser Pro Ser Ala Thr Ser Tyr Ser Gly Ser Leu Val Phe
 195 200 205

<210> 211
 <211> 1368

<212> DNA

<213> Glycine max

<220>

<223> G3810 Predicted polypeptide sequence is orthologous to G922

<400> 211

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gctggtaacc ttgaaaatgc aaacaccaca cttgagcaaa tttccatgct tgcttcccct      180
gatggggaca ctatgcagcg aatcgcaaca tattttatgg agtcgcttgc tgatcggatt      240
cttaaaacat ggcctgggat ccacagagcc ctcaactcaa ccagaatgac tttgatatcc      300
gacgaaattc tgggttcagaa gcttttcttt gagcttttcc ctttcttgaa ggtagcattt      360
gttctcacia atcaggccat cattgaagca atggaagggg agaaagtgat tcacataatt      420
gatctcaatg ctgctgaagc tgctcagtgg attgctctcc ttcgagtatt aagtgcgcat      480
cccgaaggcc ctctcattt gagaatcacc ggggttcacg agaaaaagga gattctggat      540
gaggtggctc atagactaac tgaagaagca gaaaagttgg atataccgtt ccaattcaac      600
cctgtggcaa gcaaattaga aaatcttgat tttgacaaac ttcgggtgaa aactggggag      660
gcactagcaa taagttccat tctccaattg catacccttt tggcctggga tgatgaagcc      720
atgcagagaa agtctcctct tctgttaaaa agctcaaagc gaattcacct gcaaagagtt      780
ctgccaatgg gccaaagcac attgggtgat ttgcttgaga aagatatggt taatgggtac      840
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cccagggggc gcttttctta tgccttggtg ggattatcac caaagggtcat ggttggtgaca      960
gaacaagact gtaatcacia tgggtccaact ctgatggata ggcttcttga agctctatac     1020
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ttaaggggtg agaagatgct ttttggggag gaaataaaga acatcattgc atgtgagggg     1140
totgaacgaa aggaaagaca tgaaaagctg gaaaagtggg tccagagatt tgatctagct     1200
gggtttggca acgtgccttt gagctacttt ggtatggtgc aagcaaggag gttcctgcag     1260
agctatgggt gtgaaggata cagaatgagg gatgaaaatg gttgtgtggt aatttgctgg     1320
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<210> 212

<211> 455

<212> PRT

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<220>

<223> G3810 polypeptide Orthologous to G922

<400> 212

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Met Met Ser Leu Ser Pro Ser Leu Gly Ser Pro Asn Asn Leu Leu Phe
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Arg Glu Met Lys Ser Glu Glu Arg Gly Leu Tyr Leu Ile His Leu Leu
20 25 30

Leu Thr Cys Ala Asn His Val Ala Ala Gly Asn Leu Glu Asn Ala Asn
35 40 45

Thr Thr Leu Glu Gln Ile Ser Met Leu Ala Ser Pro Asp Gly Asp Thr
50 55 60

Met Gln Arg Ile Ala Thr Tyr Phe Met Glu Ser Leu Ala Asp Arg Ile
65 70 75 80

Leu Lys Thr Trp Pro Gly Ile His Arg Ala Leu Asn Ser Thr Arg Met
85 90 95

Thr Leu Ile Ser Asp Glu Ile Leu Val Gln Lys Leu Phe Phe Glu Leu
100 105 110

Phe Pro Phe Leu Lys Val Ala Phe Val Leu Thr Asn Gln Ala Ile Ile
115 120 125

Glu Ala Met Glu Gly Glu Lys Val Ile His Ile Ile Asp Leu Asn Ala
130 135 140

Ala Glu Ala Ala Gln Trp Ile Ala Leu Leu Arg Val Leu Ser Ala His
145 150 155 160

Pro Glu Gly Pro Pro His Leu Arg Ile Thr Gly Val His Gln Lys Lys
165 170 175

Glu Ile Leu Asp Glu Val Ala His Arg Leu Thr Glu Glu Ala Glu Lys
180 185 190

Leu Asp Ile Pro Phe Gln Phe Asn Pro Val Ala Ser Lys Leu Glu Asn
195 200 205

Leu Asp Phe Asp Lys Leu Arg Val Lys Thr Gly Glu Ala Leu Ala Ile
210 215 220

Ser Ser Ile Leu Gln Leu His Thr Leu Leu Ala Trp Asp Asp Glu Ala
225 230 235 240

Met Gln Arg Lys Ser Pro Leu Leu Leu Lys Ser Ser Asn Gly Ile His
245 250 255

MBI0058CIP.ST25.txt

Leu Gln Arg Val Leu Pro Met Gly Gln Ser Thr Leu Gly Asp Leu Leu
260 265 270

Glu Lys Asp Met Val Asn Gly Tyr Thr Pro Ser Pro Asp Ser Thr Ser
275 280 285

Ser Ser Pro Ser Ser Leu Thr Thr Ser Asn Ser Arg Pro Arg Gly Arg
290 295 300

Phe Leu Asn Ala Leu Trp Gly Leu Ser Pro Lys Val Met Val Val Thr
305 310 315 320

Glu Gln Asp Cys Asn His Asn Gly Pro Thr Leu Met Asp Arg Leu Leu
325 330 335

Glu Ala Leu Tyr Ser Tyr Ala Ala Leu Phe Asp Cys Leu Glu Ser Thr
340 345 350

Val Ser Arg Thr Ser Leu Glu Arg Leu Arg Val Glu Lys Met Leu Phe
355 360 365

Gly Glu Glu Ile Lys Asn Ile Ile Ala Cys Glu Gly Ser Glu Arg Lys
370 375 380

Glu Arg His Glu Lys Leu Glu Lys Trp Phe Gln Arg Phe Asp Leu Ala
385 390 395 400

Gly Phe Gly Asn Val Pro Leu Ser Tyr Phe Gly Met Val Gln Ala Arg
405 410 415

Arg Phe Leu Gln Ser Tyr Gly Cys Glu Gly Tyr Arg Met Arg Asp Glu
420 425 430

Asn Gly Cys Val Leu Ile Cys Trp Glu Asp Arg Pro Met Tyr Ser Ile
435 440 445

Ser Ala Trp Arg Ser Arg Lys
450 455

<210> 213
<211> 1563
<212> DNA
<213> Glycine max

<220>
<223> G3811 Predicted polypeptide sequence is orthologous to G922

<400> 213
gaattcggct cgaggttattc ttctgtaact tcttcacctc ttcagttcctt ttccatgatg 60

tctctgtcag tttcacctag cttaggatct ccctaccata tgaaatgcga gcttaggggt 120
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cagcgaattg cttcttatgt ttctgaagca ctcgctgacg ggatacttaa aacatggcct 300
ggcatccaca gggccctcaa ttccagcaga ataactatgg tttctgatga aattcttgtt 360
caaaagctct tctttgagct tttacccttc ctcaagttct catatatcct cactaatcag 420
gctattgttg aagccatgga aggggagaaa atgggtgcata tagttgatct ctatggggcc 480
ggaccggcac agtggatttc tctcctccaa gttttgagtg cacgtcctga aggtcctccc 540
catttgagaa tcaccggggg ccatcacaag aaagagggttc tggatcagat ggctcataaa 600
ctcactgaag aggcggaaaa gttggatatc ccattccaat tcaaccctgt gctaagcaag 660
ttggaaaatc ttgatttcaa caaacttcgc gttaaaaactg gggaggcact ggcaataagt 720
tctattatgc agttgcactc ccttttggcc ttggatgaag atgcctcgcg gagaaaatcg 780
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ccagcagcgt cttcatctgc tttgatgaat tcggagagct ttcttaatgc cttgtggggg 960
ttatcccaa aagtcatggg tgtaactgaa caagacttta accacaactg tttgaccatg 1020
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gaatgtggtc ggggtgatgat atgctggcag gagcgatcct tgttttccat aacagcttgg 1380
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ttttaagttt ttcttttctt ttctttgttt ctaattgtat gacagagttt taccaatgtg 1500
gtaatgacta gtaatgaaga gatacttcta tttccttaaa aaaaaaaaaa aaagggcggc 1560
cgc 1563

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<210> 214
 <211> 446
 <212> PRT
 <213> Glycine max

<220>
 <223> G3811 polypeptide Orthologous to G922

<400> 214

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 20 25 30
 Ala Asn Phe Val Ala Thr Gly Asp Leu Gln Tyr Ala Tyr Leu Thr Leu
 35 40 45
 Glu Gln Ile Ser Gln His Ala Ser Leu Asp Gly Asp Thr Met Gln Arg
 50 55 60
 Ile Ala Ser Tyr Val Ser Glu Ala Leu Ala Asp Arg Ile Leu Lys Thr
 65 70 75 80
 Trp Pro Gly Ile His Arg Ala Leu Asn Ser Ser Arg Ile Thr Met Val
 85 90 95
 Ser Asp Glu Ile Leu Val Gln Lys Leu Phe Phe Glu Leu Leu Pro Phe
 100 105 110
 Leu Lys Phe Ser Tyr Ile Leu Thr Asn Gln Ala Ile Val Glu Ala Met
 115 120 125
 Glu Gly Glu Lys Met Val His Ile Val Asp Leu Tyr Gly Ala Gly Pro
 130 135 140
 Ala Gln Trp Ile Ser Leu Leu Gln Val Leu Ser Ala Arg Pro Glu Gly
 145 150 155 160
 Pro Pro His Leu Arg Ile Thr Gly Val His His Lys Lys Glu Val Leu
 165 170 175
 Asp Gln Met Ala His Lys Leu Thr Glu Glu Ala Glu Lys Leu Asp Ile
 180 185 190
 Pro Phe Gln Phe Asn Pro Val Leu Ser Lys Leu Glu Asn Leu Asp Phe
 195 200 205
 Asn Lys Leu Arg Val Lys Thr Gly Glu Ala Leu Ala Ile Ser Ser Ile
 210 215 220
 Met Gln Leu His Ser Leu Leu Ala Leu Asp Glu Asp Ala Ser Arg Arg
 225 230 235 240
 Lys Ser Pro Leu Leu Ser Lys Asn Ser Asn Ala Ile His Leu Gln Lys
 245 250 255
 Gly Leu Leu Met Asn His Asn Thr Leu Gly Asp Leu Leu Asp Gly Tyr
 260 265 270

Ser Pro Ser Pro Asp Ser Ala Ser Ser Ser Pro Ala Ala Ser Ser Ser
275 280 285

Ala Leu Met Asn Ser Glu Ser Phe Leu Asn Ala Leu Trp Gly Leu Ser
290 295 300

Pro Lys Val Met Val Val Thr Glu Gln Asp Phe Asn His Asn Cys Leu
305 310 315 320

Thr Met Met Glu Arg Leu Ala Glu Ala Leu Phe Ser Tyr Ala Ala Tyr
325 330 335

Phe Asp Cys Leu Glu Ser Thr Val Ser Arg Ala Ser Met Asp Arg Leu
340 345 350

Lys Leu Glu Lys Met Leu Phe Gly Glu Glu Ile Lys Asn Ile Ile Ala
355 360 365

Cys Glu Gly Cys Glu Arg Lys Glu Arg His Glu Lys Met Asp Arg Trp
370 375 380

Ile Gln Arg Leu Asp Leu Ser Gly Phe Ala Asn Val Pro Ile Ser Tyr
385 390 395 400

Tyr Gly Met Leu Gln Gly Arg Arg Phe Leu Gln Thr Tyr Gly Cys Glu
405 410 415

Gly Tyr Lys Met Arg Glu Glu Cys Gly Arg Val Met Ile Cys Trp Gln
420 425 430

Glu Arg Ser Leu Phe Ser Ile Thr Ala Trp Arg Pro Arg Lys
435 440 445

<210> 215

<211> 1329

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3813 Predicted polypeptide sequence is orthologous to G922

<400> 215

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aacatgccgc tccacccggc cgcgggcgcg tcgcccacgc cgccatggat ggtgcgggag 120

ctgcgttccg acgagcgcg gctgtgcctc atccatctcc tgctcaactg cgccgcggcg 180

gcggcgggccg ggcggttgga tgctgcgaac gccgcgctcg agcacatcgc gtcgctggcg 240

gcgcccgcgc gggacgccat gcagcgcggtg gcggccgcct tcgcggaggc gctggcgcg 300

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<210> 216
 <211> 442
 <212> PRT
 <213> Oryza sativa (japonica cultivar-group)

<220>
 <223> G3813 polypeptide Orthologous to G922

<400> 216

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His Asn Phe Ser Asn Met Pro Leu His Pro Ala Ala Ala Ala Ser Pro
 20 25 30

Thr Pro Pro Trp Met Val Arg Glu Leu Arg Ser Asp Glu Arg Gly Leu
 35 40 45

Cys Leu Ile His Leu Leu Leu Asn Cys Ala Ala Ala Ala Ala Gly
 50 55 60

MBI0058CIP.ST25.txt

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Arg Leu Asp Ala Ala Asn Ala Ala Leu Glu His Ile Ala Ser Leu Ala
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Ala Pro Asp Gly Asp Ala Met Gln Arg Val Ala Ala Ala Phe Ala Glu
                               85                               90                               95

Ala Leu Ala Arg Arg Ala Leu Arg Ala Trp Pro Gly Leu Cys Arg Ala
                               100                              105                              110

Leu Leu Leu Pro Arg Ala Ser Pro Thr Pro Ala Glu Val Ala Ala Ala
                               115                              120                              125

Arg Arg His Phe Leu Asp Leu Cys Pro Phe Leu Arg Leu Ala Gly Ala
                               130                              135                              140

Ala Ala Asn Gln Ser Ile Leu Glu Ala Met Glu Ser Glu Lys Ile Val
145                               150                              155                              160

His Val Ile Asp Leu Gly Gly Ala Asp Ala Thr Gln Trp Leu Glu Leu
                               165                              170                              175

Leu His Leu Leu Ala Ala Arg Pro Glu Gly Pro Pro His Leu Arg Leu
                               180                              185                              190

Thr Ser Val His Glu His Lys Glu Leu Leu Thr Gln Thr Ala Met Ala
                               195                              200                              205

Leu Thr Lys Glu Ala Glu Arg Leu Asp Val Pro Phe Gln Phe Asn Pro
                               210                              215                              220

Val Val Ser Arg Leu Asp Ala Leu Asp Val Glu Ser Leu Arg Val Lys
225                               230                              235                              240

Thr Gly Glu Ala Leu Ala Ile Cys Ser Ser Leu Gln Leu His Cys Leu
                               245                              250                              255

Leu Ala Ser Asp Asp Asp Ala Ala Ala Val Ala Gly Gly Asp Lys Glu
                               260                              265                              270

Arg Arg Ser Pro Glu Ser Gly Leu Ser Pro Ser Thr Ser Arg Ala Asp
                               275                              280                              285

Ala Phe Leu Gly Ala Leu Trp Gly Leu Ser Pro Lys Val Met Val Val
                               290                              295                              300

Ala Glu Gln Glu Ala Ser His Asn Ala Ala Gly Leu Thr Glu Arg Phe
305                               310                              315                              320

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MBI0058CIP.ST25.txt

Val Glu Ala Leu Asn Tyr Tyr Ala Ala Leu Phe Asp Cys Leu Glu Val
325 330 335

Gly Ala Ala Arg Gly Ser Val Glu Arg Ala Arg Val Glu Arg Trp Leu
340 345 350

Leu Gly Glu Glu Ile Lys Asn Ile Val Ala Cys Asp Gly Gly Glu Arg
355 360 365

Arg Glu Arg His Glu Arg Leu Glu Arg Trp Ala Arg Arg Leu Glu Gly
370 375 380

Ala Gly Phe Gly Arg Val Pro Leu Ser Tyr Tyr Ala Leu Leu Gln Ala
385 390 395 400

Arg Arg Val Ala Gln Gly Leu Gly Cys Asp Gly Phe Lys Val Arg Glu
405 410 415

Glu Lys Gly Asn Phe Phe Leu Cys Trp Gln Asp Arg Ala Leu Phe Ser
420 425 430

Val Ser Ala Trp Arg Gly Arg Arg Phe Asp
435 440

<210> 217
<211> 1554
<212> DNA
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3814 Predicted polypeptide sequence is orthologous to G922

<400> 217
atgttccagg acgacatgct gtcgtcggcg acgtcatcgc cggcgtcgtc ggtgtactcg 60
ccgtcgccgt cgccgtcgaa cgggtcgtgg gtgcaggagc tgagccatga ccagcagagc 120
gttcggctga tcggcctgct ttaccagtgc gccgccgagg tgtccgccgg ctccttcgac 180
cgcgccaacc tctgcctcga gcacatcacg cagctcgcgt ccctggacgc gccgcacgcg 240
ctccagcgcc tcgccgccgt cttcgccgac gcgctcgcgc gcaagctgct caacctcatc 300
ctgggcctct cgcgcgcgct gctgtcgtcg gccaaactccg ccgacgcca ctcgtcccc 360
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aaccatgcca tccttgaggc aatggagggg gagagggttcg tccacgtcgt cgacttctcc 480
ggcccggcgg cgaaccgggt gcagtggatc gcgctgttcc acgcgttccg aggccgccgg 540
gaaggccgc cgcacctccg catcaccgcc gtccacgaca gcaaggagtt cctcgccaac 600
atggccgcgg tgctgtccaa ggaggcggag gcgttcgaca tcgcgttcca gttcaacgcc 660
gtggaggcga agctcgacga gatggacttc gacgcgtcc gccacgacct cggcgtcagg 720

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tccggcgagg cgctcgccgt cagcgtcgtg ctgcagcttc accgcctcct cgccgtcgac      780
gacgggagga ggcacgccgc cgccggctgc ctcaccccg g tccagatcat cgcgcgctcc      840
agccccagaa gcttcggcga gctgctggag cgggagctga acacgcggct gcagctgagc      900
cccgcgcgt ccgtggtgtc gtcgctgtca cccactccc ccgcagcagc aacggcggcg      960
caccgcacga cgtcgacgcc aaagctgggg agcttcctgt cggcggtgag gtcgctgtcc     1020
ccgaagatca tggatgatgac ggagcaggag gcgaaccaca acggcggcgc gttccaggag     1080
cggttcgacg aggcgctcaa ctactacgcg tcgctgttcg actgcctgca gcggagcgcg     1140
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<210> 218

<211> 517

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3814 polypeptide Orthologous to G922

<400> 218

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Ser Val Tyr Ser Pro Ser Pro Ser Pro Ser Asn Gly Ser Trp Val Gln
          20           25           30

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```

Glu Leu Ser His Asp Gln Gln Ser Val Arg Leu Ile Gly Leu Leu Tyr
          35           40           45

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Gln Cys Ala Ala Glu Val Ser Ala Gly Ser Phe Asp Arg Ala Asn Leu
          50           55           60

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Cys Leu Glu His Ile Thr Gln Leu Ala Ser Leu Asp Ala Pro His Ala
        65           70           75           80

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Leu Gln Arg Leu Ala Ala Val Phe Ala Asp Ala Leu Ala Arg Lys Leu
          85           90           95

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Leu Asn Leu Ile Leu Gly Leu Ser Arg Ala Leu Leu Ser Ser Ala Asn
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 Ser Ala Asp Ala His Leu Val Pro Val Ala Arg Arg His Met Phe Asp
 115 120 125
 Val Leu Pro Phe Leu Lys Leu Ala Tyr Leu Thr Thr Asn His Ala Ile
 130 135 140
 Leu Glu Ala Met Glu Gly Glu Arg Phe Val His Val Val Asp Phe Ser
 145 150 155 160
 Gly Pro Ala Ala Asn Pro Val Gln Trp Ile Ala Leu Phe His Ala Phe
 165 170 175
 Arg Gly Arg Arg Glu Gly Pro Pro His Leu Arg Ile Thr Ala Val His
 180 185 190
 Asp Ser Lys Glu Phe Leu Ala Asn Met Ala Ala Val Leu Ser Lys Glu
 195 200 205
 Ala Glu Ala Phe Asp Ile Ala Phe Gln Phe Asn Ala Val Glu Ala Lys
 210 215 220
 Leu Asp Glu Met Asp Phe Asp Ala Leu Arg His Asp Leu Gly Val Arg
 225 230 235 240
 Ser Gly Glu Ala Leu Ala Val Ser Val Val Leu Gln Leu His Arg Leu
 245 250 255
 Leu Ala Val Asp Asp Gly Arg Arg His Ala Ala Ala Gly Cys Leu Thr
 260 265 270
 Pro Val Gln Ile Ile Ala Arg Ser Ser Pro Arg Ser Phe Gly Glu Leu
 275 280 285
 Leu Glu Arg Glu Leu Asn Thr Arg Leu Gln Leu Ser Pro Asp Ala Ser
 290 295 300
 Val Val Ser Ser Leu Ser Pro His Ser Pro Ala Ala Ala Thr Ala Ala
 305 310 315 320
 His Pro Thr Thr Ser Thr Pro Lys Leu Gly Ser Phe Leu Ser Ala Val
 325 330 335
 Arg Ser Leu Ser Pro Lys Ile Met Val Met Thr Glu Gln Glu Ala Asn
 340 345 350

MBI0058CIP.ST25.txt

His Asn Gly Gly Ala Phe Gln Glu Arg Phe Asp Glu Ala Leu Asn Tyr
355 360 365

Tyr Ala Ser Leu Phe Asp Cys Leu Gln Arg Ser Ala Ala Ala Ala Ala
370 375 380

Glu Arg Ala Arg Val Glu Arg Val Leu Leu Gly Glu Glu Ile Arg Gly
385 390 395 400

Val Val Ala Cys Glu Gly Ala Glu Arg Val Glu Arg His Glu Arg Ala
405 410 415

Arg Gln Trp Ala Ala Arg Met Glu Ala Ala Gly Met Glu Arg Val Gly
420 425 430

Leu Ser Tyr Ser Gly Ala Met Glu Ala Arg Lys Leu Leu Gln Ser Cys
435 440 445

Gly Trp Ala Gly Pro Tyr Glu Val Arg His Asp Ala Gly Gly His Gly
450 455 460

Phe Phe Phe Cys Trp His Lys Arg Pro Leu Tyr Ala Val Thr Ala Trp
465 470 475 480

Arg Pro Ala Ala Ser Arg Arg Gly His Thr Leu His Gly Arg Arg Ser
485 490 495

Glu Gly Thr Arg Glu Ser Val Pro Trp Pro Pro Arg Ser Arg Arg Arg
500 505 510

Cys Gly Arg Ala Arg
515

<210> 219
<211> 1401
<212> DNA
<213> Lycopersicon esculentum

<220>
<223> G3824 Predicted polypeptide sequence is orthologous to G922

<400> 219
tggagataacc atgcaaagga ttgcttcata ttttactgag gctttagctg ataggattct 60
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agaaattcctt gtttaggaaga tgtttttcga gatctttcct ttcttgaagg tggcgtttgt 180
ggtcacaaat caagctataa ttgaagctat ggaaggtgaa aagatgggtc atattgtgga 240
tcttaatgct gctgaacccc tgcaatggcg tgcgttgctt caggacttga gcgcgcgtcc 300
tgaaggaccg ccccatctgc gcattactgg gggtcatcag caaaaagagg tgttagatca 360

MBI0058CIP.ST25.txt

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aatggcacat gtgcttactc aagaagcaga aaaactggat atcccttttc agttcaatca 420
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tcttgcgatt agttcaatta tgcaattgca cacccttcta gcccatgata atgacaagaa 540
gtcccccttg ccttttaagc attcaaattg tggttaactta aacagggcac tagtcaacca 600
aaatacttta ggggaatttc ttgaaaaaga tatggctaata gggtgcagtc caagcaatga 660
caccgcttct tcatccccgc tatgttcaac tggttcaaca aagatggata gtttcctcaa 720
tgctttgtgg gggttatcac caaaagttat ggtggttaaca gaacaagatg ctaaccataa 780
tgggacaact cttatggaga ggctatcaga gtcgttacat ttttatgctg cattatttga 840
ttgtcttgaa tcgacgctgc caagaacatc attagagaga ttaaagggtg aaaagatgtt 900
attaggtgaa gagattagaa acattatagc atgtgaaggg atcgaacgaa aggagaggca 960
tgaaaagctc gaaaagtggg tccaaagatt cgacacatct gggtttggga atgtgccttt 1020
gagttattat gctatgttgc aggcaagaag gttgttgcag agttacagtt gtgaaggata 1080
caagatcaaa gaagataatg gttgcgtggg gatatgctgg caggatcgcc cacttttctc 1140
agtgtcgtct tggcgatgta ggaagtgaga ctaaacttag ttttcattgt aatgttttag 1200
atttgtatct tccttttgtt gttgtaacat aatgtgtaga actccagttg gtgaaactgc 1260
tattgacatg tttgagacat tttgtcaact tttttgatct catgtgataa gcttctctct 1320
agtgtttaga tttccatttt gatatggatc aataaagctg atgttctctt aaaaaaaaaa 1380
aaaaaaaaact cgagactagg a 1401

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<210> 220
 <211> 385
 <212> PRT
 <213> Lycopersicon esculentum

<220>
 <223> G3824 polypeptide Orthologous to G922

<400> 220

Met Gln Arg Ile Ala Ser Tyr Phe Thr Glu Ala Leu Ala Asp Arg Ile
 1 5 10 15

Leu Arg Ser Trp Pro Gly Leu Tyr Lys Ala Leu Arg Ser Thr Lys Leu
 20 25 30

Ser Val Val Ser Glu Glu Ile Leu Val Arg Lys Met Phe Phe Glu Ile
 35 40 45

Phe Pro Phe Leu Lys Val Ala Phe Val Val Thr Asn Gln Ala Ile Ile
 50 55 60

MBI0058CIP.ST25.txt

Glu Ala Met Glu Gly Glu Lys Met Val His Ile Val Asp Leu Asn Ala
65 70 75 80

Ala Glu Pro Leu Gln Trp Arg Ala Leu Leu Gln Asp Leu Ser Ala Arg
85 90 95

Pro Glu Gly Pro Pro His Leu Arg Ile Thr Gly Val His Gln Gln Lys
100 105 110

Glu Val Leu Asp Gln Met Ala His Val Leu Thr Gln Glu Ala Glu Lys
115 120 125

Leu Asp Ile Pro Phe Gln Phe Asn Gln Val Val Ser Arg Leu Glu Asn
130 135 140

Leu Asp Val Glu Lys Leu Arg Val Lys Thr Gly Glu Ala Leu Ala Ile
145 150 155 160

Ser Ser Ile Met Gln Leu His Thr Leu Leu Ala His Asp Asn Asp Lys
165 170 175

Lys Ser Pro Leu Pro Phe Lys His Ser Asn Gly Val Asn Leu Asn Arg
180 185 190

Ala Leu Val Asn Gln Asn Thr Leu Gly Glu Phe Leu Glu Lys Asp Met
195 200 205

Ala Asn Gly Cys Ser Pro Ser Asn Asp Thr Ala Ser Ser Ser Pro Leu
210 215 220

Cys Ser Thr Gly Ser Thr Lys Met Asp Ser Phe Leu Asn Ala Leu Trp
225 230 235 240

Gly Leu Ser Pro Lys Val Met Val Val Thr Glu Gln Asp Ala Asn His
245 250 255

Asn Gly Thr Thr Leu Met Glu Arg Leu Ser Glu Ser Leu His Phe Tyr
260 265 270

Ala Ala Leu Phe Asp Cys Leu Glu Ser Thr Leu Pro Arg Thr Ser Leu
275 280 285

Glu Arg Leu Lys Val Glu Lys Met Leu Leu Gly Glu Glu Ile Arg Asn
290 295 300

Ile Ile Ala Cys Glu Gly Ile Glu Arg Lys Glu Arg His Glu Lys Leu
305 310 315 320

MBI0058CIP.ST25.txt

Glu Lys Trp Phe Gln Arg Phe Asp Thr Ser Gly Phe Gly Asn Val Pro
325 330 335

Leu Ser Tyr Tyr Ala Met Leu Gln Ala Arg Arg Leu Leu Gln Ser Tyr
340 345 350

Ser Cys Glu Gly Tyr Lys Ile Lys Glu Asp Asn Gly Cys Val Val Ile
355 360 365

Cys Trp Gln Asp Arg Pro Leu Phe Ser Val Ser Ser Trp Arg Cys Arg
370 375 380

Lys
385

<210> 221
<211> 1269
<212> DNA
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3827 Predicted polypeptide sequence is orthologous to G922

<400> 221
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agagagggat gtaccagatc tggaagctcc cgccgtcagc cgcccgagg tgccgcagcc 180
gctctggccg tagccagcgc cccttcactc gcgagttggt gtcgtcgccc ctccatccgc 240
aagctgctgt cgttgccgct ccacgctcgc ccggtgccgc cgccaggctc cgggatgcgg 300
cagccgctcc gcccgtcgcc ggccggccctc caccacagag gtgctgccgt cgccctacg 360
cgctcgccctg gtgccgccgt cgccggcgct gagatgcggc agcaggtgag ctactgctgg 420
cgccctgtcc gcccgccacc ggccgggtggg gaggaggctg gcggggagct cctcctgcgc 480
ggccgcgagc tcctgctgct gcagctgctg ctaattttatc tcgtgtggga cggagggacg 540
ctgctcctcc ttgagctgag cttttcttct cttctctttt gttcacttgt gacggccatg 600
gcgctcacga aagaagcaga gcgcctcgac gtgcccttcc agttcaaccc ggtggtgtcc 660
cgccctgatg ccctcgatgt ggagtcctc cgccggctgt cactgaaggat gatggtggtg 720
acggagcagg aggtgagcca caacgcggcg gggctgacgg agcgggttcgt ggaggctctc 780
aactactacg cggcggttgt cgactgcctg gaggtgggcg gggcgcgcg gtcgggtggag 840
cgccgcgcgc tggagcgggt gctactcggg gaggagatca agaacatcgt ggcgtgtgac 900
ggcgggcgagc ggccgggagcg gcacgagcgg ctggaggggcg ccggcttttg ccgcgtcccc 960
ctcagctact acgcgctgct tcaggccagg cgggtgggcg aggggtctcg ctgcgacggc 1020
ttcaaggctc gggaggagaa gggcaacttc ttcctctgct ggcaagatcg cgccctcttc 1080

tccgtctccg catggcgcgg ccgccgcttc gccgccttgcc gccatcgacg 1140
 cctctccccct gctcccgcggt cattgctacc ttgctctcct ccccgccgcc gccttgctct 1200
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 agagagtag 1269

<210> 222
 <211> 422
 <212> PRT
 <213> Oryza sativa (japonica cultivar-group)

<220>
 <223> G3827 polypeptide Orthologous to G922

<400> 222

Met Ile Thr Phe Gly Leu Asn Ser Arg Pro His Pro Glu Phe Arg Asn
 1 5 10 15

Asp Leu Arg Pro Ser Ser Ser Ser Leu Ala Ala Gly Glu Ser Glu Ser
 20 25 30

Pro Lys Ala Val Glu Arg Leu Glu Arg Glu Gly Cys Thr Arg Ser Gly
 35 40 45

Ser Ser Arg Arg Gln Pro Arg Arg Gly Ala Ala Ala Ala Leu Ala Val
 50 55 60

Ala Ser Ala Pro Ser Leu Ala Ser Cys Cys Arg Arg Pro Ser Ile Arg
 65 70 75 80

Lys Leu Leu Ser Leu Pro Leu His Ala Arg Pro Val Pro Pro Pro Gly
 85 90 95

Ser Gly Met Arg Gln Pro Leu Arg Pro Ser Pro Ala Ala Leu His Pro
 100 105 110

Arg Gly Ala Ala Val Ala Pro Thr Arg Ser Pro Gly Ala Ala Val Ala
 115 120 125

Gly Ala Glu Met Arg Gln Gln Val Ser Tyr Cys Trp Arg Pro Val Arg
 130 135 140

Pro Pro Pro Ala Gly Gly Glu Glu Ala Gly Gly Glu Leu Leu Leu Arg
 145 150 155 160

Gly Arg Glu Leu Leu Leu Leu Gln Leu Leu Leu Ile Tyr Leu Val Trp
 165 170 175

MBI0058CIP.ST25.txt

Asp Gly Gly Thr Leu Leu Leu Leu Glu Leu Ser Ile Phe Phe Leu Leu
180 185 190

Phe Cys Ser Leu Val Thr Ala Met Ala Leu Thr Lys Glu Ala Glu Arg
195 200 205

Leu Asp Val Pro Phe Gln Phe Asn Pro Val Val Ser Arg Leu Asp Ala
210 215 220

Leu Asp Val Glu Ser Leu Arg Gly Leu Ser Leu Lys Val Met Val Val
225 230 235 240

Thr Glu Gln Glu Val Ser His Asn Ala Ala Gly Leu Thr Glu Arg Phe
245 250 255

Val Glu Ala Leu Asn Tyr Tyr Ala Ala Leu Phe Asp Cys Leu Glu Val
260 265 270

Gly Gly Ala Arg Gly Ser Val Glu Arg Thr Arg Val Glu Arg Trp Leu
275 280 285

Leu Gly Glu Glu Ile Lys Asn Ile Val Ala Cys Asp Gly Gly Glu Arg
290 295 300

Arg Glu Arg His Glu Arg Leu Glu Gly Ala Gly Phe Gly Arg Val Pro
305 310 315 320

Leu Ser Tyr Tyr Ala Leu Leu Gln Ala Arg Arg Val Ala Gln Gly Leu
325 330 335

Gly Cys Asp Gly Phe Lys Val Arg Glu Glu Lys Gly Asn Phe Phe Leu
340 345 350

Cys Trp Gln Asp Arg Ala Leu Phe Ser Val Ser Ala Trp Arg Gly Arg
355 360 365

Arg Phe Ala Ala Leu Leu Pro Leu Pro Pro Ser Thr Pro Leu Pro Cys
370 375 380

Ser Arg Val Ile Ala Thr Leu Leu Ser Ser Pro Pro Pro Pro Cys Ser
385 390 395 400

Pro Leu His Pro Tyr Cys Pro Glu Arg Arg Glu Arg Met Lys Gly Glu
405 410 415

Lys Lys Gly Lys Arg Glu
420

<210> 223
 <211> 2217
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> misc_feature
 <222> (2192)..(2192)
 <223> n is a, c, g, or t

<220>
 <223> G175 reference sequence; predicted polypeptide sequence is paralogous to G1274

<400> 223
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 gagaaaacaa attgaaactt ttttgtttgt tagagagtta aggagaaatt ttatctaacc 120
 aagctgtgta aatctcttgt agtttttctg ccgatataca ttttcattgt gttgagggta 180
 aacgataatc aagaacgaga gagagagaga gcaagagcaa gagatttcta ctacagaaga 240
 tttattatat tgatcatttt gtgtgatcaa cccataaaaa cagagagaca tagacaagtc 300
 catgtttcga tgtttcgatc tctcttactg tctaaacggc gaaataaaaa gtctgatggg 360
 tgtcacttat tgcattgata ttagtaaact agcttgagcc caagttaaag ctgaaacttg 420
 ggtttgcaat ggctggtatt gataataaag ctgctgtaat gggagaatgg ttcgactgta 480
 gtactactaa ccacaggaag agatcgaaag cggaacttgg tagagagttt tctttaaatt 540
 acatcaagaa tgaggattct ttgcaaacca cctttcaaga aagttcacga ggagctcttc 600
 gtgaaaggat tgctgcgaga tccgggttta atgcaccgtg gttaaacact gaggatattc 660
 ttcagtcgaa atctttaacc atctcttctc ctggtcttag tcctgcaact ctgttagagt 720
 ctctgtttt cctctcaaac cctttgctat ctccaacaac cgggaagctc tcatcagtac 780
 cttctgataa ggctaaagct gagttatttg acgacattac cacatcctta gccttccaaa 840
 ccatttcagg aagtggcctt gatcctacta acatcgcttt agaaccgat gattcccaag 900
 actatgaaga aagacagctc ggcgggttag gagactcgat ggcttggtgt gcacctgcag 960
 atgatggata caactggaga aaatatggac aaaagctagt taaaggaagt gagtatccgc 1020
 ggagctatta caagtgcacg caccgaatt gtgaggccaa gaagaagggt gaacggcttc 1080
 gggaaggtca tattatagag atcatataca caggagatca tatacacagc aaacctccac 1140
 ctaaccgccg gtcagggatt ggatcatccg gtactggcca agacatgcaa atagatgcaa 1200
 ccgaatacga aggttttgct ggaaccaatg agaacataga atggacatca cctgtatctg 1260
 cagagctcga atacggaagc cattcaggat caatgcaggt tcaaaacggg actcatcagt 1320
 tcgggtatgg tgatgcagca gctgatgcct tatatagaga tgaaaacgaa gatgatcgca 1380
 cgtcccacat gagtgtttcc ctgacttacg atggagaggt agaagagtcc gaatcaaaga 1440

MBI0058CIP.ST25.txt

gaaggaaact agaagcttat gcaacagaaa cgagtggatc aaccagagcc agccgtgagc 1500
 caagagttgt ggtgcagacc acaagtgaca ttgacatcct cgatgatggt tatcgctggc 1560
 gcaagtatgg gcaaaaagtc gttaaaggaa acccgaatcc aaggagctac tataaatgca 1620
 cagctaattgg atgtaccgta acgaagcatg tagagagagc ctctgatgac ttcaagagcg 1680
 tactaacaac ttatataggg aagcacaccc acgttgtacc agcagcacgc aacagcagcc 1740
 acgtcgggtgc aggcagttca gggactctcc aaggcagttt agcgactcag acccacaacc 1800
 acaatgtgca ctatccaatg ccacacagta gatctgaggg actggccaca gccaaactcat 1860
 ctctattttga cttccagtca cacctgaggg atcctacagg tttctccggt tacataggcc 1920
 aatctgagct ttctgatctt tcaatgcctg gtctaactat tgggcaagag aagcttacca 1980
 gcctgcaggc gcctgacatt ggggatccaa ctggcctaata gttgcagtta gcagcacagc 2040
 cgaaggtgga accagtgtca ccacaacagg gacttgattt gtcagcgagc tcattgatat 2100
 gcagagagat gttgagtaga ttacgacaga tatgaaacaa atctctttgt tcaactgattg 2160
 ctcaaatttt tgaataaatg aaaaattgag anaaaaaaaa aaaaaaaaaa aaaaaaa 2217

<210> 224

<211> 568

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G175 polypeptide reference sequence; paralogous to G1274

<400> 224

Met Ala Gly Ile Asp Asn Lys Ala Ala Val Met Gly Glu Trp Phe Asp
 1 5 10 15

Cys Ser Thr Thr Asn His Arg Lys Arg Ser Lys Ala Glu Leu Gly Arg
 20 25 30

Glu Phe Ser Leu Asn Tyr Ile Lys Asn Glu Asp Ser Leu Gln Thr Thr
 35 40 45

Phe Gln Glu Ser Ser Arg Gly Ala Leu Arg Glu Arg Ile Ala Ala Arg
 50 55 60

Ser Gly Phe Asn Ala Pro Trp Leu Asn Thr Glu Asp Ile Leu Gln Ser
 65 70 75 80

Lys Ser Leu Thr Ile Ser Ser Pro Gly Leu Ser Pro Ala Thr Leu Leu
 85 90 95

Glu Ser Pro Val Phe Leu Ser Asn Pro Leu Leu Ser Pro Thr Thr Gly
 100 105 110

MBI0058CIP.ST25.txt

Lys Leu Ser Ser Val Pro Ser Asp Lys Ala Lys Ala Glu Leu Phe Asp
 115 120 125
 Asp Ile Thr Thr Ser Leu Ala Phe Gln Thr Ile Ser Gly Ser Gly Leu
 130 135 140
 Asp Pro Thr Asn Ile Ala Leu Glu Pro Asp Asp Ser Gln Asp Tyr Glu
 145 150 155 160
 Glu Arg Gln Leu Gly Gly Leu Gly Asp Ser Met Ala Cys Cys Ala Pro
 165 170 175
 Ala Asp Asp Gly Tyr Asn Trp Arg Lys Tyr Gly Gln Lys Leu Val Lys
 180 185 190
 Gly Ser Glu Tyr Pro Arg Ser Tyr Tyr Lys Cys Thr His Pro Asn Cys
 195 200 205
 Glu Ala Lys Lys Lys Val Glu Arg Ser Arg Glu Gly His Ile Ile Glu
 210 215 220
 Ile Ile Tyr Thr Gly Asp His Ile His Ser Lys Pro Pro Pro Asn Arg
 225 230 235 240
 Arg Ser Gly Ile Gly Ser Ser Gly Thr Gly Gln Asp Met Gln Ile Asp
 245 250 255
 Ala Thr Glu Tyr Glu Gly Phe Ala Gly Thr Asn Glu Asn Ile Glu Trp
 260 265 270
 Thr Ser Pro Val Ser Ala Glu Leu Glu Tyr Gly Ser His Ser Gly Ser
 275 280 285
 Met Gln Val Gln Asn Gly Thr His Gln Phe Gly Tyr Gly Asp Ala Ala
 290 295 300
 Ala Asp Ala Leu Tyr Arg Asp Glu Asn Glu Asp Asp Arg Thr Ser His
 305 310 315 320
 Met Ser Val Ser Leu Thr Tyr Asp Gly Glu Val Glu Glu Ser Glu Ser
 325 330 335
 Lys Arg Arg Lys Leu Glu Ala Tyr Ala Thr Glu Thr Ser Gly Ser Thr
 340 345 350
 Arg Ala Ser Arg Glu Pro Arg Val Val Val Gln Thr Thr Ser Asp Ile
 355 360 365

MBI0058CIP.ST25.txt

Asp Ile Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Val
370 375 380

Val Lys Gly Asn Pro Asn Pro Arg Ser Tyr Tyr Lys Cys Thr Ala Asn
385 390 395 400

Gly Cys Thr Val Thr Lys His Val Glu Arg Ala Ser Asp Asp Phe Lys
405 410 415

Ser Val Leu Thr Thr Tyr Ile Gly Lys His Thr His Val Val Pro Ala
420 425 430

Ala Arg Asn Ser Ser His Val Gly Ala Gly Ser Ser Gly Thr Leu Gln
435 440 445

Gly Ser Leu Ala Thr Gln Thr His Asn His Asn Val His Tyr Pro Met
450 455 460

Pro His Ser Arg Ser Glu Gly Leu Ala Thr Ala Asn Ser Ser Leu Phe
465 470 475 480

Asp Phe Gln Ser His Leu Arg His Pro Thr Gly Phe Ser Val Tyr Ile
485 490 495

Gly Gln Ser Glu Leu Ser Asp Leu Ser Met Pro Gly Leu Thr Ile Gly
500 505 510

Gln Glu Lys Leu Thr Ser Leu Gln Ala Pro Asp Ile Gly Asp Pro Thr
515 520 525

Gly Leu Met Leu Gln Leu Ala Ala Gln Pro Lys Val Glu Pro Val Ser
530 535 540

Pro Gln Gln Gly Leu Asp Leu Ser Ala Ser Ser Leu Ile Cys Arg Glu
545 550 555 560

Met Leu Ser Arg Leu Arg Gln Ile
565

<210> 225

<211> 1072

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G303 reference sequence

<400> 225

aaaagataac gtagccatta acttttatgc attaactcct tcatttcctt ttgtgctcgt

60

MBI0058CIP.ST25.txt

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ttggttgaga gagagagagg ctatatatga tgttccaaca agattaccct catggctttt 120
cactcgtgga aacatcctta agttacgaaa tgttggatta ctttcaaaac atcgtcgttt 180
cgaactctga agacgtggcg tcacagcaaa attccatttc gtcctcttct tattcatcag 240
cgacactctc ctgctccata acagagcaaa aatctcactt aactgaaaag ttatctcctc 300
tacgagaaaag atatggttgc ggtgactttc tgtcgcggaa gaggagaagg agaagtgaaa 360
aaacgattgt agataaagag aatcaaagga tgaatcacat tgccgtcgag cgtaaccgga 420
gaaaacagat gaatcatttt ctgtctatcc tcaagtctat gatgcctctc tcttattctc 480
aacctaataa ccaagcatca atcatagaag ggaccattag ctatctgaag aagctagaac 540
aacgtctcca atctctcgaa gcccaattaa aagctactaa actcaatcaa tcaccaaata 600
tattttccga cttcttcatg ttccctcaat actccaccgc cactgccact gccaccgcca 660
ctgcctcctc atcctcctcg agccaccacc atcacaagcg actagagggtg gttgctgacg 720
tgagggttac aatggtagaa agacatgcca acattaaagt gttaacgaag acacagccaa 780
gattgctctt caagattatc aatgagttta actcttttagg ttttaagtact cttcatctca 840
acctcacaac ttccaaagac atgtctctct tcacttttag cgtcaaggta gaggcagatt 900
gtcaattgac gccttctggg aatgaggtcg caaatacggg gcatgaagtc gttagaagag 960
ttcacaagga acgttgaatt ttgtttacat actagctaac tttgaaattc tattttattg 1020
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<210> 226

<211> 296

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G303 polypeptide reference sequence

<400> 226

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Met Met Phe Gln Gln Asp Tyr Pro His Gly Phe Ser Leu Val Glu Thr
1          5          10          15

```

```

Ser Leu Ser Tyr Glu Met Leu Asp Tyr Phe Gln Asn Ile Val Val Ser
20          25          30

```

```

Asn Ser Glu Asp Val Ala Ser Gln Gln Asn Ser Ile Ser Ser Ser Ser
35          40          45

```

```

Tyr Ser Ser Ala Thr Leu Ser Cys Ser Ile Thr Glu Gln Lys Ser His
50          55          60

```

```

Leu Thr Glu Lys Leu Ser Pro Leu Arg Glu Arg Tyr Gly Cys Gly Asp
65          70          75          80

```

MBI0058CIP.ST25.txt

Phe Leu Ser Arg Lys Arg Arg Arg Arg Ser Glu Lys Thr Ile Val Asp
85 90 95

Lys Glu Asn Gln Arg Met Asn His Ile Ala Val Glu Arg Asn Arg Arg
100 105 110

Lys Gln Met Asn His Phe Leu Ser Ile Leu Lys Ser Met Met Pro Leu
115 120 125

Ser Tyr Ser Gln Pro Asn Asp Gln Ala Ser Ile Ile Glu Gly Thr Ile
130 135 140

Ser Tyr Leu Lys Lys Leu Glu Gln Arg Leu Gln Ser Leu Glu Ala Gln
145 150 155 160

Leu Lys Ala Thr Lys Leu Asn Gln Ser Pro Asn Ile Phe Ser Asp Phe
165 170 175

Phe Met Phe Pro Gln Tyr Ser Thr Ala Thr Ala Thr Ala Thr Ala Thr
180 185 190

Ala Ser Ser Ser Ser Ser Ser His His His His Lys Arg Leu Glu Val
195 200 205

Val Ala Asp Val Glu Val Thr Met Val Glu Arg His Ala Asn Ile Lys
210 215 220

Val Leu Thr Lys Thr Gln Pro Arg Leu Leu Phe Lys Ile Ile Asn Glu
225 230 235 240

Phe Asn Ser Leu Gly Leu Ser Thr Leu His Leu Asn Leu Thr Thr Ser
245 250 255

Lys Asp Met Ser Leu Phe Thr Phe Ser Val Lys Val Glu Ala Asp Cys
260 265 270

Gln Leu Thr Pro Ser Gly Asn Glu Val Ala Asn Thr Val His Glu Val
275 280 285

Val Arg Arg Val His Lys Glu Arg
290 295

<210> 227

<211> 628

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G354 reference sequence

MBI0058CIP.ST25.txt

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<400> 227
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gctgcggggg agatgaacgt gttttccgat gcaagacttg tcttaaagag ttctcatcgt      180
ttcaagcttt gggaggtcat cgtgcaagcc acaagaaact tatcaacagt gacaatccat      240
cacttcttgg atccttgtcc aacaagaaaa ctaaaacgtc tcatccttgt ccgatatgtg      300
gagtgaagtt tccgatggga caagctcttg gtggtcacat gaggagacat aggaacgaga      360
aagtctcagg ctcgttggtt acacgttctt ttctaccgga gacgacgacg gtgacggctt      420
tgaagaaatt tagtagtggg aagagagtgg cttggttggg tttggactta gattcgatgg      480
agagtttggg caattggaag ttggagttgg gaagaacgat ttcttggagt taagtttttg      540
ggttgatatac agtttcacat gattttgtaa tctttgttga tccaattatc gtaccgatcg      600
atgtgaatat tattttgata caataaaa                                         628

```

```

<210> 228
<211> 168
<212> PRT
<213> Arabidopsis thaliana

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<220>
<223> G354 polypeptide reference sequence

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<400> 228

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Met Val Ala Arg Ser Glu Glu Ile Val Ile Val Glu Glu Asp Thr Thr
1           5           10           15

```

```

Ala Lys Cys Leu Met Leu Leu Ser Arg Val Gly Glu Cys Gly Gly Gly
          20           25           30

```

```

Cys Gly Gly Asp Glu Arg Val Phe Arg Cys Lys Thr Cys Leu Lys Glu
          35           40           45

```

```

Phe Ser Ser Phe Gln Ala Leu Gly Gly His Arg Ala Ser His Lys Lys
          50           55           60

```

```

Leu Ile Asn Ser Asp Asn Pro Ser Leu Leu Gly Ser Leu Ser Asn Lys
65           70           75           80

```

```

Lys Thr Lys Thr Ser His Pro Cys Pro Ile Cys Gly Val Lys Phe Pro
          85           90           95

```

```

Met Gly Gln Ala Leu Gly Gly His Met Arg Arg His Arg Asn Glu Lys
          100          105          110

```

```

Val Ser Gly Ser Leu Val Thr Arg Ser Phe Leu Pro Glu Thr Thr Thr

```

115

120

125

Val Thr Ala Leu Lys Lys Phe Ser Ser Gly Lys Arg Val Ala Cys Leu
130 135 140

Asp Leu Asp Leu Asp Ser Met Glu Ser Leu Val Asn Trp Lys Leu Glu
145 150 155 160

Leu Gly Arg Thr Ile Ser Trp Ser
165

<210> 229
<211> 869
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G489 reference sequence

<400> 229
tggtagtgaaggatcaacaagaccatgga cagtctggag ctatgaacta tggcacaaac 60
ccataccaaa ccaaccgat gagcaccact gctgctactg tagcaggagg tgcggcacia 120
ccaggccagc tggcggtcca ccagatccat cagcagcagc agcagcaaca gctggcacag 180
cagcttcaag cattttggga gaaccaattc aaagagattg agaagactac cgatttcaag 240
aaccacagcc ttccccttgc gagaatcaag aaaatcatga aagcggatga agatgtccgt 300
atgatctcgg ctgaggcgcc ggtcgtgttt gcaagggcct gtgagatgtt catcctggag 360
ctgacactca ggtcgtggaa ccacactgag gagaataaga ggcgagcgtt gcagaagaac 420
gatattgctg ctgctgtgac tagaaccgat atttttgatt tccttgtgga tattgttccc 480
cgaggaggatc tccgagatga agtcttggga agtattccga ggggcactgt cccggaagct 540
gctgctgctg gttacccgta tggatacttg cctgcaggaa ctgctccaat aggaaatccg 600
ggaatgggta tgggtaatcc cgggtggtgcg tatccaccta atccttatat ggggtcaacca 660
atgtggcaac aacaggcacc tgaccaacct gaccaggaaa attagcaaga aactgtgagt 720
cttcagctt cttttaggcc taccttgtag tcttgggggtt ttgtttctgt tttcgaataa 780
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tattcttatc ttattgaagt aaaaatgtg 869

<210> 230
<211> 220
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G489 polypeptide reference sequence

<400> 230

MBI0058CIP.ST25.txt

Met Asn Tyr Gly Thr Asn Pro Tyr Gln Thr Asn Pro Met Ser Thr Thr
1 5 10 15

Ala Ala Thr Val Ala Gly Gly Ala Ala Gln Pro Gly Gln Leu Ala Phe
20 25 30

His Gln Ile His Gln Gln Gln Gln Gln Gln Leu Ala Gln Gln Leu
35 40 45

Gln Ala Phe Trp Glu Asn Gln Phe Lys Glu Ile Glu Lys Thr Thr Asp
50 55 60

Phe Lys Asn His Ser Leu Pro Leu Ala Arg Ile Lys Lys Ile Met Lys
65 70 75 80

Ala Asp Glu Asp Val Arg Met Ile Ser Ala Glu Ala Pro Val Val Phe
85 90 95

Ala Arg Ala Cys Glu Met Phe Ile Leu Glu Leu Thr Leu Arg Ser Trp
100 105 110

Asn His Thr Glu Glu Asn Lys Arg Arg Thr Leu Gln Lys Asn Asp Ile
115 120 125

Ala Ala Ala Val Thr Arg Thr Asp Ile Phe Asp Phe Leu Val Asp Ile
130 135 140

Val Pro Arg Glu Asp Leu Arg Asp Glu Val Leu Gly Ser Ile Pro Arg
145 150 155 160

Gly Thr Val Pro Glu Ala Ala Ala Ala Gly Tyr Pro Tyr Gly Tyr Leu
165 170 175

Pro Ala Gly Thr Ala Pro Ile Gly Asn Pro Gly Met Val Met Gly Asn
180 185 190

Pro Gly Gly Ala Tyr Pro Pro Asn Pro Tyr Met Gly Gln Pro Met Trp
195 200 205

Gln Gln Gln Ala Pro Asp Gln Pro Asp Gln Glu Asn
210 215 220

<210> 231

<211> 798

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G634 reference sequence

```

<400> 231
atggagcaag gaggaggtgg tgggtgtaat gaagttgtgg aggaagcttc acctattagt      60
tcaagacctc ctgctaacaa cttagaagag cttatgagat tctcagccgc cgcggatgac      120
ggtggattag gaggtggagg tggaggagga ggaggaggaa gtgcttcttc ttcacgga      180
aatcgatggc cgagagaaga aacttttagct cttcttcgga tccgatccga tatggattct      240
acttttcgtg atgctactct caaagctcct ctttggaac atgtttccag gaagctattg      300
gagttaggtt acaaacgaag ttcaaagaaa tgcaaagaga aattcgaaaa cgttcagaaa      360
tattacaaac gtactaaaga aactcgcggt ggtcgtcatg atggtaaagc ttacaagttc      420
ttctctcagc ttgaagctct caacactact cctcctcctc ctccttctca tcctcacgct      480
catcaaccag aacagaaaaca acaacaacaa ccacaacaag agatgggtcat gagctcggaa      540
caatcatcat taccatcatc atcaagatgg ccaaaggcag agattctagc gcttataaac      600
ctgagaagtg gaatggaacc aaggtaccaa gataatgtac ctaaaggact tctatgggaa      660
gagatctcaa cttcaatgaa gagaatggga tacaacagaa acgctaagag atgtaaagag      720
aaatgggaaa acataaacia atactacaag aaagttaaag aaagcaacaa cagcaactac      780
aacaacaaga atcaatga                                     798

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<210> 232
<211> 265
<212> PRT
<213> Arabidopsis thaliana

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```

<220>
<223> G634 polypeptide reference sequence

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```

<400> 232

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```

Met Glu Gln Gly Gly Gly Gly Gly Gly Asn Glu Val Val Glu Glu Ala
1          5          10          15

```

```

Ser Pro Ile Ser Ser Arg Pro Pro Ala Asn Asn Leu Glu Glu Leu Met
          20          25          30

```

```

Arg Phe Ser Ala Ala Ala Asp Asp Gly Gly Leu Gly Gly Gly Gly Gly
          35          40          45

```

```

Gly Gly Gly Gly Gly Ser Ala Ser Ser Ser Ser Gly Asn Arg Trp Pro
          50          55          60

```

```

Arg Glu Glu Thr Leu Ala Leu Leu Arg Ile Arg Ser Asp Met Asp Ser
65          70          75          80

```

```

Thr Phe Arg Asp Ala Thr Leu Lys Ala Pro Leu Trp Glu His Val Ser
          85          90          95

```


MBI0058CIP.ST25.txt

Arg Lys Leu Leu Glu Leu Gly Tyr Lys Arg Ser Ser Lys Lys Cys Lys
100 105 110

Glu Lys Phe Glu Asn Val Gln Lys Tyr Tyr Lys Arg Thr Lys Glu Thr
115 120 125

Arg Gly Gly Arg His Asp Gly Lys Ala Tyr Lys Phe Phe Ser Gln Leu
130 135 140

Glu Ala Leu Asn Thr Thr Pro Pro Pro Pro Pro Ser His Pro His Ala
145 150 155 160

His Gln Pro Glu Gln Lys Gln Gln Gln Gln Pro Gln Gln Glu Met Val
165 170 175

Met Ser Ser Glu Gln Ser Ser Leu Pro Ser Ser Ser Arg Trp Pro Lys
180 185 190

Ala Glu Ile Leu Ala Leu Ile Asn Leu Arg Ser Gly Met Glu Pro Arg
195 200 205

Tyr Gln Asp Asn Val Pro Lys Gly Leu Leu Trp Glu Glu Ile Ser Thr
210 215 220

Ser Met Lys Arg Met Gly Tyr Asn Arg Asn Ala Lys Arg Cys Lys Glu
225 230 235 240

Lys Trp Glu Asn Ile Asn Lys Tyr Tyr Lys Lys Val Lys Glu Ser Asn
245 250 255

Asn Ser Asn Tyr Asn Asn Lys Asn Gln
260 265

<210> 233

<211> 341

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G682 reference sequence

<400> 233

acatggataa ccatcgcagg actaagcaac ccaagaccaa ctccatcggt acttcttctt 60

ctgaaggaac agaagtgagt agtcttgagt gggaagttgt gaacatgagt caagaagaag 120

aagatttggt ctctcgaatg cataagcttg tcggtgacag gtgggaactg atagctggga 180

ggatcccagg aagaaccgct ggagaaattg agagggttttg ggtcatgaaa aattgaaaag 240

tgatcaatat atctctatag tttcactgat tgtttcgatt atattccggt gtatttttaa 300

tttaccaact ctgttataag aagaaaactt tcttaaactc c

341

<210> 234

<211> 77

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G682 polypeptide reference sequence

<400> 234

Met	Asp	Asn	His	Arg	Arg	Thr	Lys	Gln	Pro	Lys	Thr	Asn	Ser	Ile	Val
1				5					10					15	

Thr	Ser	Ser	Ser	Glu	Gly	Thr	Glu	Val	Ser	Ser	Leu	Glu	Trp	Glu	Val
			20					25					30		

Val	Asn	Met	Ser	Gln	Glu	Glu	Glu	Asp	Leu	Val	Ser	Arg	Met	His	Lys
		35					40					45			

Leu	Val	Gly	Asp	Arg	Trp	Glu	Leu	Ile	Ala	Gly	Arg	Ile	Pro	Gly	Arg
	50						55				60				

Thr	Ala	Gly	Glu	Ile	Glu	Arg	Phe	Trp	Val	Met	Lys	Asn
65					70					75		

<210> 235

<211> 1797

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G916 reference sequence

<400> 235

aaaaaaaaa acaatctaag atatctatca agatcttaag atatctacat ttatagagat	60
gtttcgtttt ccggttaagtc ttggaggagg tccacgtgag aatctgaagc catcagatga	120
gcagcatcaa cgtgcggtgg tgaatgaggt tgactttttc cgatcagcgg agaagagaga	180
tagggtttca cgtgaagaac aaaacattat cgccgatgag actcataggg ttcattgtcaa	240
aagggagaat tcacgtgttg atgatcatga cgatcgttct actgatcaca tcaatattgg	300
acttaatctt ctactgcga atacgggaag cgacgagtca atggtggatg atggattgtc	360
tgtggatatg gaagagaaac gtacaaagtg tgagaatgca caacttcgcg aagagctaaa	420
gaaggcgagt gaagataatc aaagactaaa gcaaatgcta agtcaaacaa ccaacaactt	480
caattccttg cagatgcaac ttgttgctgt catgaggcaa caagaagatc atcatcacct	540
agctacgacc gagaacaatg acaatgtaaa gaaccgacat gaagtgcctg aaatggttcc	600
aagacagttc atcgatttgg gaccgcattc tgacgaagtg tcgtccgagg agaggacgac	660

MBI0058CIP.ST25.txt

```

ggttcggtcg ggatctcctc cctcgcttct agagaaatct agctcacgtc aaaacggaaa 720
gagagtgctt gtaagagaag aaagcccgga aaccgaatcc aacggctgga gaaaccctaa 780
caaagttcct aaacaccatg catcatccag catttgcggt ggcaatggca gtgaaaatgc 840
aagtagcaag gtcattgagc aagcggccgc cgaagccacc atgcgtaaag cccgtgtctc 900
ggttcgtgct cgatccgaag ctcccatgtt aagcgatgga tgtcaatgga gaaaatacgg 960
acaaaaaatg gcgaaaggaa acccggtgcc tcgagcttat taccggtgca caatggctgt 1020
tggtatgtct gttcgcaagc aagtgaacg ttgcgcggaa gatagaacca ttctcataac 1080
aacctacgaa ggaaaccata accatccatt acctcctgcg gctatgaaca tggcttcaac 1140
tacaacagca gccgcaagca tgcttctctc aggtccacc atgtcgaacc aagacggttt 1200
aatgaaccca acaaattctt tggtcgaac catattaccg tgttctcaa gcatggctac 1260
tatctcagcc tctgcacat tcccaacat tacattagac ctcacagagt cacccaacgg 1320
gaacaatcca accaataacc cgctgatgca attctctcaa cggctctggt tgggtggagt 1380
gaaccaatcg gttttgcctc atatgatggg tcaggctttg tactacaacc aacagtctaa 1440
gttttcgggt ttacatatgc cgtctcagcc gctaaacgt ggtgagagtg ttagcgccgc 1500
tactgccgca atcgctcca atcccaactt tgccgcggct ctagctgcag ccataacttc 1560
gattatcaac ggttcgaaca atcagcagaa tgggaacaac aataacagta atgttacaac 1620
gagcaacgtt gacaataggc aataacattt tttataagt tttagttagg gactttttat 1680
cggtcgattt tgttttgttt ttcttttatt acattatttt ttagttacgg cttttttttg 1740
ttttttcttt tctttcccaa acaacaagta ttgagagcaa tccccccccc cccccct 1797

```

<210> 236

<211> 528

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G916 polypeptide reference sequence

<400> 236

```

Met Phe Arg Phe Pro Val Ser Leu Gly Gly Gly Pro Arg Glu Asn Leu
1           5           10           15

```

```

Lys Pro Ser Asp Glu Gln His Gln Arg Ala Val Val Asn Glu Val Asp
          20           25           30

```

```

Phe Phe Arg Ser Ala Glu Lys Arg Asp Arg Val Ser Arg Glu Glu Gln
          35           40           45

```

```

Asn Ile Ile Ala Asp Glu Thr His Arg Val His Val Lys Arg Glu Asn
          50           55           60

```

MBI0058CIP.ST25.txt

Ser Arg Val Asp Asp His Asp Asp Arg Ser Thr Asp His Ile Asn Ile
65 70 75 80

Gly Leu Asn Leu Leu Thr Ala Asn Thr Gly Ser Asp Glu Ser Met Val
85 90 95

Asp Asp Gly Leu Ser Val Asp Met Glu Glu Lys Arg Thr Lys Cys Glu
100 105 110

Asn Ala Gln Leu Arg Glu Glu Leu Lys Lys Ala Ser Glu Asp Asn Gln
115 120 125

Arg Leu Lys Gln Met Leu Ser Gln Thr Thr Asn Asn Phe Asn Ser Leu
130 135 140

Gln Met Gln Leu Val Ala Val Met Arg Gln Gln Glu Asp His His His
145 150 155 160

Leu Ala Thr Thr Glu Asn Asn Asp Asn Val Lys Asn Arg His Glu Val
165 170 175

Pro Glu Met Val Pro Arg Gln Phe Ile Asp Leu Gly Pro His Ser Asp
180 185 190

Glu Val Ser Ser Glu Glu Arg Thr Thr Val Arg Ser Gly Ser Pro Pro
195 200 205

Ser Leu Leu Glu Lys Ser Ser Ser Arg Gln Asn Gly Lys Arg Val Leu
210 215 220

Val Arg Glu Glu Ser Pro Glu Thr Glu Ser Asn Gly Trp Arg Asn Pro
225 230 235 240

Asn Lys Val Pro Lys His His Ala Ser Ser Ser Ile Cys Gly Gly Asn
245 250 255

Gly Ser Glu Asn Ala Ser Ser Lys Val Ile Glu Gln Ala Ala Ala Glu
260 265 270

Ala Thr Met Arg Lys Ala Arg Val Ser Val Arg Ala Arg Ser Glu Ala
275 280 285

Pro Met Leu Ser Asp Gly Cys Gln Trp Arg Lys Tyr Gly Gln Lys Met
290 295 300

Ala Lys Gly Asn Pro Cys Pro Arg Ala Tyr Tyr Arg Cys Thr Met Ala
305 310 315 320

MBI0058CIP.ST25.txt

Val Gly Cys Pro Val Arg Lys Gln Val Gln Arg Cys Ala Glu Asp Arg
325 330 335

Thr Ile Leu Ile Thr Thr Tyr Glu Gly Asn His Asn His Pro Leu Pro
340 345 350

Pro Ala Ala Met Asn Met Ala Ser Thr Thr Thr Ala Ala Ala Ser Met
355 360 365

Leu Leu Ser Gly Ser Thr Met Ser Asn Gln Asp Gly Leu Met Asn Pro
370 375 380

Thr Asn Leu Leu Ala Arg Thr Ile Leu Pro Cys Ser Ser Ser Met Ala
385 390 395 400

Thr Ile Ser Ala Ser Ala Pro Phe Pro Thr Ile Thr Leu Asp Leu Thr
405 410 415

Glu Ser Pro Asn Gly Asn Asn Pro Thr Asn Asn Pro Leu Met Gln Phe
420 425 430

Ser Gln Arg Ser Gly Leu Val Glu Leu Asn Gln Ser Val Leu Pro His
435 440 445

Met Met Gly Gln Ala Leu Tyr Tyr Asn Gln Gln Ser Lys Phe Ser Gly
450 455 460

Leu His Met Pro Ser Gln Pro Leu Asn Ala Gly Glu Ser Val Ser Ala
465 470 475 480

Ala Thr Ala Ala Ile Ala Ser Asn Pro Asn Phe Ala Ala Ala Leu Ala
485 490 495

Ala Ala Ile Thr Ser Ile Ile Asn Gly Ser Asn Asn Gln Gln Asn Gly
500 505 510

Asn Asn Asn Asn Ser Asn Val Thr Thr Ser Asn Val Asp Asn Arg Gln
515 520 525

<210> 237

<211> 768

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G975 reference sequence

<400> 237

attactcatc atcaagttcc tacttttctct ctgacaaaaca tcacagagta agtaagaatg

60

MBI0058CIP.ST25.txt

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attcgctcatc ctctcttgaa acggaggatt tggctagga cgttcgagac cgcagaggag 180
gcagcaagag catacgacga ggccgccgtt ttaatgagcg gccgcaacgc caaaaccaac 240
tttccctca acaacaacaa caccggagaa acttccgagg gcaaaaccga tatttcagct 300
tcgtccacaa tgtcatctc aacatcatct tcatcgctct cttccatcct cagcgccaaa 360
ctgaggaaat gctgcaagtc tccttccccca tccctcacct gcctccgtct tgacacagcc 420
agctcccata tcggcgctctg gcagaaacgg gccggttcaa agtctgactc cagctgggtc 480
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gacgctattc ttgctccgac cactgaagtt gaaattggtg gcagcagaga agaagtattg 600
gatgaggaag aaaaggttgc tttgcaaatg atagaggagc ttctcaatac aaactaaatc 660
ttatttgctt atatatatgt acctattttc attgctgatt tacagccaaa ataatcaatt 720
ataccgtgta ttttatagat gttttatatt aaaaggttgt tagatata 768

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<210> 238

<211> 199

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G975 polypeptide reference sequence

<400> 238

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Met Val Gln Thr Lys Lys Phe Arg Gly Val Arg Gln Arg His Trp Gly
1           5           10           15

```

```

Ser Trp Val Ala Glu Ile Arg His Pro Leu Leu Lys Arg Arg Ile Trp
          20           25           30

```

```

Leu Gly Thr Phe Glu Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Glu
35           40           45

```

```

Ala Ala Val Leu Met Ser Gly Arg Asn Ala Lys Thr Asn Phe Pro Leu
50           55           60

```

```

Asn Asn Asn Asn Thr Gly Glu Thr Ser Glu Gly Lys Thr Asp Ile Ser
65           70           75           80

```

```

Ala Ser Ser Thr Met Ser Ser Ser Thr Ser Ser Ser Ser Leu Ser Ser
          85           90           95

```

```

Ile Leu Ser Ala Lys Leu Arg Lys Cys Cys Lys Ser Pro Ser Pro Ser
100          105          110

```

```

Leu Thr Cys Leu Arg Leu Asp Thr Ala Ser Ser His Ile Gly Val Trp

```

115

120

125

Gln Lys Arg Ala Gly Ser Lys Ser Asp Ser Ser Trp Val Met Thr Val
 130 135 140

Glu Leu Gly Pro Ala Ser Ser Ser Gln Glu Thr Thr Ser Lys Ala Ser
 145 150 155 160

Gln Asp Ala Ile Leu Ala Pro Thr Thr Glu Val Glu Ile Gly Gly Ser
 165 170 175

Arg Glu Glu Val Leu Asp Glu Glu Glu Lys Val Ala Leu Gln Met Ile
 180 185 190

Glu Glu Leu Leu Asn Thr Asn
 195

<210> 239

<211> 1116

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G1069 Reference sequence; functionally related, homologous to G1073

<400> 239

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 ttttagcgggc atggtggacc attcgggtctc ctcaggccat caccaaaacc atcaccacca 180
 aagtcttctt accaaaggag atcttgggaat agccatgaat cagagccaag acaacgacca 240
 agacgaagaa gatgatacta gagaaggagc cggtgaggtg gtcaaccgta gaccaagagg 300
 tagaccacca ggatccaaaa acaaacccaa agctccaata tttgtgacaa gagacagccc 360
 caacgcactc cgtagccatg tcttggagat ctccgacggc agtgacgtcg ccgacacaat 420
 cgctcacttc tcaagacgca ggcaacgcgg cgtttgcggt ctcagcggga caggctcagt 480
 cgctaacgta accctccgcc aagccgccgc accaggaggt gtggtctctc tccaaggcag 540
 gtttgaaatc ttatctttaa ccggtgcttt cctccctgga ccttccccac ccgggtcaac 600
 cggtttaacg gtttacttag ccgggggtcca gggtcagggt gttggaggta gcgttgtagg 660
 cccactctta gccatagggg cggtcatggt gattgctgct actttctcta acgctactta 720
 tgagagattg cccatggaag aagaggaaga cggtggcggc tcaagacaga ttcacggagg 780
 cggtgactca ccgcccagaa tcggtagtaa cctgcctgat ctatcaggga tggccggggc 840
 aggctacaat atgccgccgc atctgattcc aaatggggct ggtagcctag ggcacgaacc 900
 atatacatgg gtccacgcaa gaccacctta ctgactcagt gagccatttc tatatataat 960

MBI0058CIP.ST25.txt

gggtctatata aataaatata tagatgaata taagcaagca atttgaggta gtctattaca 1020
aagcttttgc tctggttgga aaaataaata agtatcaaag ctttgtttgt tcttaatgga 1080
aatatagagc ttgggaaggt agaaagagac gacatt 1116

<210> 240
<211> 281
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> Reference sequence; functionally related, homologous to G1073

<400> 240

Met Ala Asn Pro Trp Trp Thr Asn Gln Ser Gly Leu Ala Gly Met Val
1 5 10 15

Asp His Ser Val Ser Ser Gly His His Gln Asn His His His Gln Ser
20 25 30

Leu Leu Thr Lys Gly Asp Leu Gly Ile Ala Met Asn Gln Ser Gln Asp
35 40 45

Asn Asp Gln Asp Glu Glu Asp Asp Pro Arg Glu Gly Ala Val Glu Val
50 55 60

Val Asn Arg Arg Pro Arg Gly Arg Pro Pro Gly Ser Lys Asn Lys Pro
65 70 75 80

Lys Ala Pro Ile Phe Val Thr Arg Asp Ser Pro Asn Ala Leu Arg Ser
85 90 95

His Val Leu Glu Ile Ser Asp Gly Ser Asp Val Ala Asp Thr Ile Ala
100 105 110

His Phe Ser Arg Arg Arg Gln Arg Gly Val Cys Val Leu Ser Gly Thr
115 120 125

Gly Ser Val Ala Asn Val Thr Leu Arg Gln Ala Ala Ala Pro Gly Gly
130 135 140

Val Val Ser Leu Gln Gly Arg Phe Glu Ile Leu Ser Leu Thr Gly Ala
145 150 155 160

Phe Leu Pro Gly Pro Ser Pro Pro Gly Ser Thr Gly Leu Thr Val Tyr
165 170 175

Leu Ala Gly Val Gln Gly Gln Val Val Gly Gly Ser Val Val Gly Pro
180 185 190

Leu Leu Ala Ile Gly Ser Val Met Val Ile Ala Ala Thr Phe Ser Asn
195 200 205

Ala Thr Tyr Glu Arg Leu Pro Met Glu Glu Glu Glu Asp Gly Gly Gly
210 215 220

Ser Arg Gln Ile His Gly Gly Gly Asp Ser Pro Pro Arg Ile Gly Ser
225 230 235 240

Asn Leu Pro Asp Leu Ser Gly Met Ala Gly Pro Gly Tyr Asn Met Pro
245 250 255

Pro His Leu Ile Pro Asn Gly Ala Gly Gln Leu Gly His Glu Pro Tyr
260 265 270

Thr Trp Val His Ala Arg Pro Pro Tyr
275 280

<210> 241

<211> 1371

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G1452 Reference sequence; functionally related, homologous to G512

<400> 241

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taaccacgtt atcatttttg tcttttacta tctcattaca ctcttctgtt attcgcccaa 120
ttcttacagt cactactctc tatagggtc gagcgccgc cgggcaggt ttctatgcag 180
atgggtcaca cttcccgctc cattgcccag attgggttcg gtgtaagtc gcaattagta 240
ctcactatag ggctcgagcg gccgcccggg caggtaaaag atcaaacaat gtctaaagaa 300
gctgagatgt cgatcgcggt gtcggctttg ttccctgggt ttagattctc tctactgat 360
gttgaactta tctcgtaacta tcttcgtcgt aaaatcgatg gtgatgagaa ctctgttgct 420
gtgattgctg aggtcgagat ttacaagttc gagccgtggg acttgccaga ggaatcgaaa 480
ctgaaatcgg agaacgagt gttttacttc tgcgcgaggg ggaggaagta cccgcacggg 540
tcacaaagcc ggcgagccac acagctagga tattggaaaag cgaccggtaa agagcggagt 600
gttaaattccg ggaaccaagt tgttgaacc aagagaacgc ttgtatttca tatcggtcgg 660
gtcctcgtg gcgagagaac ggagtggatt atgcatgaat actgcatcca tggagcccca 720
caggatgcat tagtggtgtg ccggttaaga aaaaatgctg attttcgggc tagttcgacc 780
caaaaaattg aggatggtgt tgtgcaagac gatggctacg ttggccaaag aggtggtttg 840
gacaaggagg acaaatccta ctatgaatct gagcatcaga taccaaatgg tgacatcgca 900

MBI0058CIP.ST25.txt

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 ccaactaatc caactcatca agaaacaata tcaagcgagt catcgagtaa gaggtcaaaa 1080
 tgtgggtataa aaaaagaatc aacggaaaca atgaattggt acgctttgtt caggatcaag 1140
 aacgttgccg gaaccgactc cagctggaga ttcccgaacc cgttcaaaat caagaaagat 1200
 gatagccaga gattgatgaa gaatgttctg gccactactg ttttcttggc tatcttattt 1260
 tctttctttt ggactgtatt aatagctagg aactaaagct agttacgaca tacatattat 1320
 ttatacataa ataaatatag tattttgtct atggcaaaaa aaaaaaaaaa a 1371

<210> 242

<211> 373

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G1452 polypeptide Reference sequence; functionally related, homologous to G512

<400> 242

Met Gln Met Val His Thr Ser Arg Ser Ile Ala Gln Ile Gly Phe Gly
 1 5 10 15

Val Lys Ser Gln Leu Val Leu Thr Ile Gly Leu Glu Arg Pro Pro Gly
 20 25 30

Gln Val Lys Asp Gln Thr Met Ser Lys Glu Ala Glu Met Ser Ile Ala
 35 40 45

Val Ser Ala Leu Phe Pro Gly Phe Arg Phe Ser Pro Thr Asp Val Glu
 50 55 60

Leu Ile Ser Tyr Tyr Leu Arg Arg Lys Ile Asp Gly Asp Glu Asn Ser
 65 70 75 80

Val Ala Val Ile Ala Glu Val Glu Ile Tyr Lys Phe Glu Pro Trp Asp
 85 90 95

Leu Pro Glu Glu Ser Lys Leu Lys Ser Glu Asn Glu Trp Phe Tyr Phe
 100 105 110

Cys Ala Arg Gly Arg Lys Tyr Pro His Gly Ser Gln Ser Arg Arg Ala
 115 120 125

Thr Gln Leu Gly Tyr Trp Lys Ala Thr Gly Lys Glu Arg Ser Val Lys
 130 135 140

MBI0058CIP.ST25.txt

Ser Gly Asn Gln Val Val Gly Thr Lys Arg Thr Leu Val Phe His Ile
145 150 155 160

Gly Arg Ala Pro Arg Gly Glu Arg Thr Glu Trp Ile Met His Glu Tyr
165 170 175

Cys Ile His Gly Ala Pro Gln Asp Ala Leu Val Val Cys Arg Leu Arg
180 185 190

Lys Asn Ala Asp Phe Arg Ala Ser Ser Thr Gln Lys Ile Glu Asp Gly
195 200 205

Val Val Gln Asp Asp Gly Tyr Val Gly Gln Arg Gly Gly Leu Asp Lys
210 215 220

Glu Asp Lys Ser Tyr Tyr Glu Ser Glu His Gln Ile Pro Asn Gly Asp
225 230 235 240

Ile Ala Glu Ser Ser Asn Val Val Glu Asp Gln Ala Asp Thr Asp Asp
245 250 255

Asp Cys Tyr Ala Glu Ile Leu Asn Asp Asp Ile Ile Lys Leu Asp Glu
260 265 270

Glu Ala Leu Lys Ala Ser Gln Ala Phe Arg Pro Thr Asn Pro Thr His
275 280 285

Gln Glu Thr Ile Ser Ser Glu Ser Ser Ser Lys Arg Ser Lys Cys Gly
290 295 300

Ile Lys Lys Glu Ser Thr Glu Thr Met Asn Cys Tyr Ala Leu Phe Arg
305 310 315 320

Ile Lys Asn Val Ala Gly Thr Asp Ser Ser Trp Arg Phe Pro Asn Pro
325 330 335

Phe Lys Ile Lys Lys Asp Asp Ser Gln Arg Leu Met Lys Asn Val Leu
340 345 350

Ala Thr Thr Val Phe Leu Ala Ile Leu Phe Ser Phe Phe Trp Thr Val
355 360 365

Leu Ile Ala Arg Asn
370

<210> 243
<211> 732
<212> DNA
<213> Arabidopsis thaliana

<220>

<223> G1820 Reference sequence

<400> 243

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gcgacaacat gaacaacgac aaccaccagc aaccaccgctc gtactcgcag ctgccgccga      120
tggcatcatc caaccctcag ttacgtaatt actggattga gcagatggaa accgtctcgg      180
atttcaaaaa ccgtcagctt ccattggctc gaattaagaa gatcatgaag gctgatccag      240
atgtgcacat ggtctccgca gaggctccga tcatcttcgc aaaggcttgc gaaatgttca      300
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agaaatcgga tatctccaac gcagtggcta gctctttcac ctacgatttc cttcttgatg      420
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ctgacgggtgg aggagtaccg caatattatt atccaccggg agtggtgatg ggaactccta      540
tggttggttag tggaatgtac gcgccatcgc aggcgtggcc agcagcggct ggtgacgggg      600
aggatgatgc tgaggataat ggaggaaacg gcggcggaaa ttgaagtgtg gatttagggt      660
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gtcggatttg ct                                     732
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<210> 244

<211> 202

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G1820 polypeptide Reference sequence

<400> 244

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1          5          10          15
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```
His Gln Gln Pro Pro Ser Tyr Ser Gln Leu Pro Pro Met Ala Ser Ser
20          25          30
```

```
Asn Pro Gln Leu Arg Asn Tyr Trp Ile Glu Gln Met Glu Thr Val Ser
35          40          45
```

```
Asp Phe Lys Asn Arg Gln Leu Pro Leu Ala Arg Ile Lys Lys Ile Met
50          55          60
```

```
Lys Ala Asp Pro Asp Val His Met Val Ser Ala Glu Ala Pro Ile Ile
65          70          75          80
```

```
Phe Ala Lys Ala Cys Glu Met Phe Ile Val Asp Leu Thr Met Arg Ser
85          90          95
```

Trp Leu Lys Ala Glu Glu Asn Lys Arg His Thr Leu Gln Lys Ser Asp
100 105 110

Ile Ser Asn Ala Val Ala Ser Ser Phe Thr Tyr Asp Phe Leu Leu Asp
115 120 125

Val Val Pro Lys Asp Glu Ser Ile Ala Thr Ala Asp Pro Gly Phe Val
130 135 140

Ala Met Pro His Pro Asp Gly Gly Gly Val Pro Gln Tyr Tyr Tyr Pro
145 150 155 160

Pro Gly Val Val Met Gly Thr Pro Met Val Gly Ser Gly Met Tyr Ala
165 170 175

Pro Ser Gln Ala Trp Pro Ala Ala Ala Gly Asp Gly Glu Asp Asp Ala
180 185 190

Glu Asp Asn Gly Gly Asn Gly Gly Gly Asn
195 200

<210> 245

<211> 866

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G2701 reference sequence; predicted polypeptide sequence is paralogous to G1634

<400> 245

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ccattctctc acctacctat ctctgaccac cggttcggtt ttcaagagat ggtgagctta	120
cacagctcga gtagcggtag ctggactaaa gaagagaaca agatgttcga acgagctctt	180
gcgatatacg ctgaagactc gcctgatcgc tggtttaaag ttgcttccat gatccctgga	240
aagactgttt ttgatgttat gaagcaatat agtaagcttg aagaagacgt tttcgatatt	300
gaagcaggac gtgttcccat tcctggttat cctgcagctt cttctccctt ggggtttgac	360
acggacatgt gtcgtaaacg gcctagtgga gctagaggat ctgatcaaga tcgaaagaaa	420
ggagtccctt ggacagagga agaacacagg agattcttgt taggccttct caagtacggt	480
aaaggagatt ggagaaacat atcgagaaac ttcgtggtgt caaagacgcc aacgcaagtg	540
gcgagccacg cccaaaagta ttaccagaga cagctctccg gagccaagga caaacgcagg	600
ccaagtatcc atgacatcac aaccggcaat cttctcaatg ccaatctcaa ccgttccttt	660
tccgatcata gagatattct ccctgattta gggtttatcg ataaggatga tacggaggag	720

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ggagtaatat ttatgggtca gaatctctct tcagaaaatc tgttttctcc atcaccaact 780
tcattcgaag ctgccattaa cttcgccgga gaaaatgtct tcagtgccgg agcttaaggc 840
aacatagaat ccccaaactc agcggc 866

<210> 246
<211> 263
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G2701 polypeptide reference sequence; paralogous to G1634

<400> 246

Met Glu Thr Leu His Pro Phe Ser His Leu Pro Ile Ser Asp His Arg
1 5 10 15

Phe Val Val Gln Glu Met Val Ser Leu His Ser Ser Ser Ser Gly Ser
20 25 30

Trp Thr Lys Glu Glu Asn Lys Met Phe Glu Arg Ala Leu Ala Ile Tyr
35 40 45

Ala Glu Asp Ser Pro Asp Arg Trp Phe Lys Val Ala Ser Met Ile Pro
50 55 60

Gly Lys Thr Val Phe Asp Val Met Lys Gln Tyr Ser Lys Leu Glu Glu
65 70 75 80

Asp Val Phe Asp Ile Glu Ala Gly Arg Val Pro Ile Pro Gly Tyr Pro
85 90 95

Ala Ala Ser Ser Pro Leu Gly Phe Asp Thr Asp Met Cys Arg Lys Arg
100 105 110

Pro Ser Gly Ala Arg Gly Ser Asp Gln Asp Arg Lys Lys Gly Val Pro
115 120 125

Trp Thr Glu Glu Glu His Arg Arg Phe Leu Leu Gly Leu Leu Lys Tyr
130 135 140

Gly Lys Gly Asp Trp Arg Asn Ile Ser Arg Asn Phe Val Val Ser Lys
145 150 155 160

Thr Pro Thr Gln Val Ala Ser His Ala Gln Lys Tyr Tyr Gln Arg Gln
165 170 175

Leu Ser Gly Ala Lys Asp Lys Arg Arg Pro Ser Ile His Asp Ile Thr
180 185 190

Thr Gly Asn Leu Leu Asn Ala Asn Leu Asn Arg Ser Phe Ser Asp His
195 200 205

Arg Asp Ile Leu Pro Asp Leu Gly Phe Ile Asp Lys Asp Asp Thr Glu
210 215 220

Glu Gly Val Ile Phe Met Gly Gln Asn Leu Ser Ser Glu Asn Leu Phe
225 230 235 240

Ser Pro Ser Pro Thr Ser Phe Glu Ala Ala Ile Asn Phe Ala Gly Glu
245 250 255

Asn Val Phe Ser Ala Gly Ala
260

<210> 247

<211> 1040

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G2789 Reference sequence; predicted polypeptide sequence is paralogous to G596

<400> 247

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tcaagtgatc atcagcacta tcaccatcaa aacgctggac gacaaaaacg cggcagagaa	180
gaagaaggag ttgaacccaa caatataggg gaagacctag ccacctttcc ttccggagaa	240
gagaatatca agaagagaag gccacgtggc agacctgctg gttccaagaa caaacccaaa	300
gcaccaatca tagtcactcg cgactccgcg aacgccttca gatgtcacgt catggagata	360
accaacgcct gcgatgtaat ggaaagccta gccgtcttcg ctagacgccg tcagcgtggc	420
gtttgcgtct tgaccggaaa cggggccggt acaaacgtca ccgtagaca acctggcgga	480
ggcgctcgta gtttacacgg acggtttgag attctttctc tctcgggttc gtttcttctt	540
ccaccggcac caccagctgc gtctggttta aagggttact tagccggtgg tcaaggtcaa	600
gtgatcggag gcagtgtggt gggaccgctt acggcatcaa gtccggtggt cgttatggca	660
gcttcatttg gaaacgcac ttacgagagg ctgccactag aggaggagga ggaaactgaa	720
agagaaatag atggaaacgc ggctagggcg attggaacgc aaacgcagaa acagttaatg	780
caagatgcga catcgtttat tgggtcgccg tcgaatttaa ttaactctgt ttcgttgcca	840
ggtgaagctt attggggaac gcaacgaccg tctttctaaag ataatatcat tgataatata	900
agtttcgtct tcttattctt tttcactttt tacctttttc actttcttag gttttgtttt	960

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 ttgcgagccg aaacgcggcc 1040

<210> 248
 <211> 265
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> G2789 polypeptide reference sequence; paralogous to G596

<400> 248

Met Asp Glu Val Ser Arg Ser His Thr Pro Gln Phe Leu Ser Ser Asp
 1 5 10 15

His Gln His Tyr His His Gln Asn Ala Gly Arg Gln Lys Arg Gly Arg
 20 25 30

Glu Glu Glu Gly Val Glu Pro Asn Asn Ile Gly Glu Asp Leu Ala Thr
 35 40 45

Phe Pro Ser Gly Glu Glu Asn Ile Lys Lys Arg Arg Pro Arg Gly Arg
 50 55 60

Pro Ala Gly Ser Lys Asn Lys Pro Lys Ala Pro Ile Ile Val Thr Arg
 65 70 75 80

Asp Ser Ala Asn Ala Phe Arg Cys His Val Met Glu Ile Thr Asn Ala
 85 90 95

Cys Asp Val Met Glu Ser Leu Ala Val Phe Ala Arg Arg Arg Gln Arg
 100 105 110

Gly Val Cys Val Leu Thr Gly Asn Gly Ala Val Thr Asn Val Thr Val
 115 120 125

Arg Gln Pro Gly Gly Gly Val Val Ser Leu His Gly Arg Phe Glu Ile
 130 135 140

Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala Pro Pro Ala Ala
 145 150 155 160

Ser Gly Leu Lys Val Tyr Leu Ala Gly Gly Gln Gly Gln Val Ile Gly
 165 170 175

Gly Ser Val Val Gly Pro Leu Thr Ala Ser Ser Pro Val Val Val Met
 180 185 190

Ala Ala Ser Phe Gly Asn Ala Ser Tyr Glu Arg Leu Pro Leu Glu Glu

195

200

205

Glu Glu Glu Thr Glu Arg Glu Ile Asp Gly Asn Ala Ala Arg Ala Ile
210 215 220

Gly Thr Gln Thr Gln Lys Gln Leu Met Gln Asp Ala Thr Ser Phe Ile
225 230 235 240

Gly Ser Pro Ser Asn Leu Ile Asn Ser Val Ser Leu Pro Gly Glu Ala
245 250 255

Tyr Trp Gly Thr Gln Arg Pro Ser Phe
260 265

<210> 249

<211> 495

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G2839 Reference sequence; predicted polypeptide sequence is paralogous to G354

<400> 249

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aaactcatta acagtagcga tccatcactt cttggatcct tgtctaacaa gaaaactaaa 240
acggcgacgt ctcaccttg tccgatatgt ggcgtggagt ttccgatggg gcaagctctt 300
gggtggtcaca tgaggagaca taggagttag aaagcctcac caggcacgtt ggttacacgt 360
tcttttttac cggagacgac gacggtagac actttgaaaa aatcgagtag tgggaagaga 420
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agaacgattt cttga 495

<210> 250

<211> 164

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G2839 polypeptide reference sequence; paralogous to G354

<400> 250

Met Val Ala Arg Ser Glu Glu Val Glu Ile Val Glu Asp Thr Ala Ala
1 5 10 15

Lys Cys Leu Met Leu Leu Ser Arg Val Gly Glu Cys Gly Gly Gly Gly
20 25 30

Glu Lys Arg Val Phe Arg Cys Lys Thr Cys Leu Lys Glu Phe Ser Ser
35 40 45

Phe Gln Ala Leu Gly Gly His Arg Ala Ser His Lys Lys Leu Ile Asn
50 55 60

Ser Ser Asp Pro Ser Leu Leu Gly Ser Leu Ser Asn Lys Lys Thr Lys
65 70 75 80

Thr Ala Thr Ser His Pro Cys Pro Ile Cys Gly Val Glu Phe Pro Met
85 90 95

Gly Gln Ala Leu Gly Gly His Met Arg Arg His Arg Ser Glu Lys Ala
100 105 110

Ser Pro Gly Thr Leu Val Thr Arg Ser Phe Leu Pro Glu Thr Thr Thr
115 120 125

Val Thr Thr Leu Lys Lys Ser Ser Ser Gly Lys Arg Val Ala Cys Leu
130 135 140

Asp Leu Asp Ser Met Glu Ser Leu Val Asn Trp Lys Leu Glu Leu Gly
145 150 155 160

Arg Thr Ile Ser

<210> 251
<211> 1569
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G2854 Reference sequence; predicted polypeptide sequence is paralogous to G1940

<400> 251
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caacaggggcc agggcagatt ccttccgacc aacaagctta cctccagcag cagcagtcgt 180
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caggatcagc tgggtgagatc cggtccttgt ggatcgggtga cttgcagcca tggatggatg 360
agaactatct catgaacgtc tttggtctta ctggcgaggc tacagcagct aaagttattc 420
gcaataaaca gaacggatat tcagaagggt atggctttat tgagtttggtg aaccatgcta 480

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acacagtttt tgttggagac ttggcacctg atgttaccga ccacatgctt actgaaacgt 660
ttaaagctgt gtattcctct gtcaagggag ctaaagttgt gaatgatagg actactggac 720
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atgaccatt 1569

<210> 252

<211> 415

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G2854 polypeptide reference sequence; paralogous to G1940

<400> 252

Met Met Gln Gln Pro Pro Pro Ala Ser Asn Gly Ala Ala Thr Gly Pro
1 5 10 15

Gly Gln Ile Pro Ser Asp Gln Gln Ala Tyr Leu Gln Gln Gln Gln Ser
20 25 30

Trp Met Met Gln His Gln Gln Gln Gln Gly Gln Pro Pro Ala Gly
35 40 45

Trp Asn Gln Gln Ser Ala Pro Ser Ser Gly Gln Pro Gln Gln Gln Gln
50 55 60

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Tyr Gly Gly Gly Gly Ser Gln Asn Pro Gly Ser Ala Gly Glu Ile Arg
 65 70 75 80
 Ser Leu Trp Ile Gly Asp Leu Gln Pro Trp Met Asp Glu Asn Tyr Leu
 85 90 95
 Met Asn Val Phe Gly Leu Thr Gly Glu Ala Thr Ala Ala Lys Val Ile
 100 105 110
 Arg Asn Lys Gln Asn Gly Tyr Ser Glu Gly Tyr Gly Phe Ile Glu Phe
 115 120 125
 Val Asn His Ala Thr Ala Glu Arg Asn Leu Gln Thr Tyr Asn Gly Ala
 130 135 140
 Pro Met Pro Ser Ser Glu Gln Ala Phe Arg Leu Asn Trp Ala Gln Leu
 145 150 155 160
 Gly Ala Gly Glu Arg Arg Gln Ala Glu Gly Pro Glu His Thr Val Phe
 165 170 175
 Val Gly Asp Leu Ala Pro Asp Val Thr Asp His Met Leu Thr Glu Thr
 180 185 190
 Phe Lys Ala Val Tyr Ser Ser Val Lys Gly Ala Lys Val Val Asn Asp
 195 200 205
 Arg Thr Thr Gly Arg Ser Lys Gly Tyr Gly Phe Val Arg Phe Ala Asp
 210 215 220
 Glu Ser Glu Gln Ile Arg Ala Met Thr Glu Met Asn Gly Gln Tyr Cys
 225 230 235 240
 Ser Ser Arg Pro Met Arg Thr Gly Pro Ala Ala Asn Lys Lys Pro Leu
 245 250 255
 Thr Met Gln Pro Ala Ser Tyr Gln Asn Thr Gln Gly Asn Ser Gly Glu
 260 265 270
 Ser Asp Pro Thr Asn Thr Thr Ile Phe Val Gly Ala Val Asp Gln Ser
 275 280 285
 Val Thr Glu Asp Asp Leu Lys Ser Val Phe Gly Gln Phe Gly Glu Leu
 290 295 300
 Val His Val Lys Ile Pro Ala Gly Lys Arg Cys Gly Phe Val Gln Tyr
 305 310 315 320

Ala Asn Arg Ala Cys Ala Glu Gln Ala Leu Ser Val Leu Asn Gly Thr
325 330 335

Gln Leu Gly Gly Gln Ser Ile Arg Leu Ser Trp Gly Arg Ser Pro Ser
340 345 350

Asn Lys Gln Thr Gln Pro Asp Gln Ala Gln Tyr Gly Gly Gly Gly Gly
355 360 365

Tyr Tyr Gly Tyr Pro Pro Gln Gly Tyr Glu Ala Tyr Gly Tyr Ala Pro
370 375 380

Pro Pro Gln Asp Pro Asn Ala Tyr Tyr Gly Gly Tyr Ala Gly Gly Gly
385 390 395 400

Tyr Gly Asn Tyr Gln Gln Pro Gly Gly Tyr Gln Gln Gln Gln Gln
405 410 415

<210> 253

<211> 914

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G3083; reference sequence

<400> 253

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gctaccggtg atgaggaacg gttaaggag gctgtggaca gagtgatgga acactttaga	180
gaatatcaca gggccaagtg ggctgcgacg gataaagacg tcatcgaagt tatggcttct	240
ccttgggctt cagctcttga acggctcgctt cagtgggtcg gtgggtggcg accaaccacc	300
ttgttccatc tgggtttacac tgagtcgagt attttatctg agtctcgtat cgttgatata	360
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cgacggctag cagaaatcgt ccaccgaact gatgatctgc gactgagaac gatcacacgt	600
gtggtggagg tcttgagtcc gctccaacaa gcggagtttc ttgtcgtcgc ggctgagctt	660
cgtaacaggcg ttgctggttg ggggactagc caccgacgtc gtcgaagttc cgaagtttaa	720
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ttaattatat gttttttacca tgtttttggt tatccagact gagtttggtt ttacatgggt	840
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<210> 254

<211> 237

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G3083 polypeptide; reference sequence

<400> 254

Met Ser Gln Glu Thr Ala Ile Ala Ser Phe Lys Lys Phe Gln Gln Ser
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Trp Ile Glu Gln Leu Arg Asn His Leu Asn His Leu Arg Ser Ala Gln
 20 25 30

Asn His His Arg Asn Ser Ala Thr Gly Asp Glu Glu Arg Leu Arg Glu
 35 40 45

Ala Val Asp Arg Val Met Glu His Phe Arg Glu Tyr His Arg Ala Lys
 50 55 60

Trp Ala Ala Thr Asp Lys Asp Val Ile Glu Val Met Ala Ser Pro Trp
 65 70 75 80

Ala Ser Ala Leu Glu Arg Ser Leu Gln Trp Val Gly Gly Trp Arg Pro
 85 90 95

Thr Thr Leu Phe His Leu Val Tyr Thr Glu Ser Ser Ile Leu Phe Glu
 100 105 110

Ser Arg Ile Val Asp Ile Leu Arg Gly Phe Arg Thr Gly Asp Leu Ser
 115 120 125

Asp Leu Ser Pro Ser Gln Phe Arg Thr Val Ser Glu Leu Gln Cys Glu
 130 135 140

Thr Val Lys Glu Glu Asn Ala Ile Thr Glu Glu Leu Ser Glu Trp Gln
 145 150 155 160

Asp Asp Ala Ser Asp Leu Val Met Gly Thr Ser Ser Asp Pro Asp Gln
 165 170 175

Arg Ile Arg Arg Leu Ala Glu Ile Val His Arg Thr Asp Asp Leu Arg
 180 185 190

Leu Arg Thr Ile Thr Arg Val Val Glu Val Leu Ser Pro Leu Gln Gln
 195 200 205

Ala Glu Phe Leu Val Ala Ala Ala Glu Leu Arg Thr Gly Val Ala Gly
 210 215 220

Trp Gly Thr Ser His Asp Arg Arg Arg Ser Ser Glu Val
 225 230 235

<210> 255
 <211> 1974
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <223> G184; predicted polypeptide sequence is paralogous to G916

<400> 255
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 caacgggtgga tgatggacta tcaatggata tggaagataa acgtgcaaag attgagaacg 660
 cacaactaca agaagagctc aagaagatga aaatagagaa tcaaaggcta agagatatgt 720
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 cggccgcaga agccaccatg cggaaagccc gtgtctcagt tcgtgcccga tctgaagctg 1200
 ccatgataag cgatggatgt caatggagaa agtacggaca aaaaatggct aaaggaaacc 1260
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 tgaacggttc cagtcacaa aataataaca ccaataataa taatgtggct acgagcaaca 1920
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<210> 256

<211> 536

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G184 polypeptide; paralogous to G916

<400> 256

Met Phe Arg Phe Pro Val Ser Leu Gly Gly Ser Arg Asp Glu Asp Arg
 1 5 10 15

His Asp Gln Ile Thr Pro Leu Asp Asp His Arg Val Val Val Asp Glu
 20 25 30

Val Asp Phe Phe Ser Glu Lys Arg Asp Arg Val Ser Arg Glu Asn Ile
 35 40 45

Asn Asp Asp Asp Asp Glu Gly Asn Lys Val Leu Ile Lys Met Glu Gly
 50 55 60

Ser Arg Val Glu Glu Asn Asp Arg Ser Arg Asp Val Asn Ile Gly Leu
 65 70 75 80

Asn Leu Leu Thr Ala Asn Thr Gly Ser Asp Glu Ser Thr Val Asp Asp
 85 90 95

Gly Leu Ser Met Asp Met Glu Asp Lys Arg Ala Lys Ile Glu Asn Ala
 100 105 110

Gln Leu Gln Glu Glu Leu Lys Lys Met Lys Ile Glu Asn Gln Arg Leu
 115 120 125

Arg Asp Met Leu Ser Gln Ala Thr Thr Asn Phe Asn Ala Leu Gln Met
 Page 236

130		135		140															
Gln	Leu	Val	Ala	Val	Met	Arg	Gln	Gln	Glu	Gln	Arg	Asn	Ser	Ser	Gln				
145					150					155					160				
Asp	His	Leu	Leu	Glu	Ser	Lys	Ala	Glu	Gly	Arg	Lys	Arg	Gln	Glu	Leu				
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Gln	Ile	Met	Val	Pro	Arg	Gln	Phe	Met	Asp	Leu	Gly	Pro	Ser	Ser	Gly				
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Ala	Ala	Glu	Ala	Thr	Met	Arg	Lys	Ala	Arg	Val	Ser	Val	Arg	Ala	Arg				
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Ser	Glu	Ala	Ala	Met	Ile	Ser	Asp	Gly	Cys	Gln	Trp	Arg	Lys	Tyr	Gly				
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Gln	Lys	Met	Ala	Lys	Gly	Asn	Pro	Cys	Pro	Arg	Ala	Tyr	Tyr	Arg	Cys				
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				325					330					335					
Glu	Asp	Arg	Ser	Ile	Leu	Ile	Thr	Thr	Tyr	Glu	Gly	Asn	His	Asn	His				
			340					345					350						
Pro	Leu	Pro	Pro	Ala	Ala	Thr	Ala	Met	Ala	Ser	Thr	Thr	Thr	Ala	Ala				
		355					360					365							
Ala	Ser	Met	Leu	Leu	Ser	Gly	Ser	Met	Ser	Ser	Gln	Asp	Gly	Leu	Met				
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385                               390                               395                               400

Met Ala Thr Ile Ser Ala Ser Ala Pro Phe Pro Thr Ile Thr Leu Asp
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Leu Thr Asn Ser Pro Asn Gly Asn Asn Pro Asn Met Thr Thr Asn Asn
                     420                               425                               430

Pro Leu Met Gln Phe Ala Gln Arg Pro Gly Phe Asn Pro Ala Val Leu
                     435                               440                               445

Pro Gln Val Val Gly Gln Ala Met Tyr Asn Asn Gln Gln Gln Ser Lys
                     450                               455                               460

Phe Ser Gly Leu Gln Leu Pro Ala Gln Pro Leu Gln Ile Ala Ala Thr
465                               470                               475                               480

Ser Ser Val Ala Glu Ser Val Ser Ala Ala Ser Ala Ala Ile Ala Ser
                     485                               490                               495

Asp Pro Asn Phe Ala Ala Ala Leu Ala Ala Ala Ile Thr Ser Ile Met
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Asn Gly Ser Ser His Gln Asn Asn Asn Thr Asn Asn Asn Asn Val Ala
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Thr Ser Asn Asn Asp Ser Arg Gln
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<210> 257

<211> 1931

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G186; predicted polypeptide sequence is paralogous to G916

<400> 257

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ggcgaagtgg atttcttctc cgacaagaaa tctagggttt gtcgtgaaga cgacgaagga      420
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<210> 258

<211> 553

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G186 polypeptide; paralogous to G916

<400> 258

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MBI0058CIP.ST25.txt

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 50 55 60
 Gly Ile Arg Asp Arg Glu Asp Glu Asp Phe Ser Ser Gly Val Ala Gly
 65 70 75 80
 Asp Asn Asp Arg Glu Val Pro Gly Glu Val Asp Phe Phe Ser Asp Lys
 85 90 95
 Lys Ser Arg Val Cys Arg Glu Asp Asp Glu Gly Phe Arg Val Lys Lys
 100 105 110
 Glu Glu Gln Asp Asp Arg Thr Asp Val Asn Thr Gly Leu Asn Leu Arg
 115 120 125
 Thr Thr Gly Asn Thr Lys Ser Asp Glu Ser Met Ile Asp Asp Gly Glu
 130 135 140
 Ser Ser Glu Met Glu Asp Lys Arg Ala Lys Asn Glu Leu Val Lys Leu
 145 150 155 160
 Gln Asp Glu Leu Lys Lys Met Thr Met Asp Asn Gln Lys Leu Arg Glu
 165 170 175
 Leu Leu Thr Gln Val Ser Asn Ser Tyr Thr Ser Leu Gln Met His Leu
 180 185 190
 Val Ser Leu Met Gln Gln Gln Gln Gln Asn Asn Lys Val Ile Glu
 195 200 205
 Ala Ala Glu Lys Pro Glu Glu Thr Ile Val Pro Arg Gln Phe Ile Asp
 210 215 220
 Leu Gly Pro Thr Arg Ala Val Gly Glu Ala Glu Asp Val Ser Asn Ser
 225 230 235 240
 Ser Ser Glu Asp Arg Thr Arg Ser Gly Gly Ser Ser Ala Ala Glu Arg
 245 250 255
 Arg Ser Asn Gly Lys Arg Leu Gly Arg Glu Glu Ser Pro Glu Thr Glu
 260 265 270

MBI0058CIP.ST25.txt

Ser Asn Lys Ile Gln Lys Val Asn Ser Thr Thr Pro Thr Thr Phe Asp
275 280 285

Gln Thr Ala Glu Ala Thr Met Arg Lys Ala Arg Val Ser Val Arg Ala
290 295 300

Arg Ser Glu Ala Pro Met Ile Ser Asp Gly Cys Gln Trp Arg Lys Tyr
305 310 315 320

Gly Gln Lys Met Ala Lys Gly Asn Pro Cys Pro Arg Ala Tyr Tyr Arg
325 330 335

Cys Thr Met Ala Thr Gly Cys Pro Val Arg Lys Gln Val Gln Arg Cys
340 345 350

Ala Glu Asp Arg Ser Ile Leu Ile Thr Thr Tyr Glu Gly Asn His Asn
355 360 365

His Pro Leu Pro Pro Ala Ala Val Ala Met Ala Ser Thr Thr Thr Ala
370 375 380

Ala Ala Asn Met Leu Leu Ser Gly Ser Met Ser Ser His Asp Gly Met
385 390 395 400

Met Asn Pro Thr Asn Leu Leu Ala Arg Ala Val Leu Pro Cys Ser Thr
405 410 415

Ser Met Ala Thr Ile Ser Ala Ser Ala Pro Phe Pro Thr Val Thr Leu
420 425 430

Asp Leu Thr His Ser Pro Pro Pro Pro Asn Gly Ser Asn Pro Ser Ser
435 440 445

Ser Ala Ala Thr Asn Asn Asn His Asn Ser Leu Met Gln Arg Pro Gln
450 455 460

Gln Gln Gln Gln Gln Met Thr Asn Leu Pro Pro Gly Met Leu Pro His
465 470 475 480

Val Ile Gly Gln Ala Leu Tyr Asn Gln Ser Lys Phe Ser Gly Leu Gln
485 490 495

Phe Ser Gly Gly Ser Pro Ser Thr Ala Ala Phe Ser Gln Ser His Ala
500 505 510

Val Ala Asp Thr Ile Thr Ala Leu Thr Ala Asp Pro Asn Phe Thr Ala
515 520 525

Ala Leu Ala Ala Val Ile Ser Ser Met Ile Asn Gly Thr Asn His His
530 535 540

Asp Gly Glu Gly Asn Asn Lys Asn Gln
545 550

<210> 259
<211> 727
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G353 Predicted polypeptide sequence is paralogous to G354

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aagttggagc ttggaagaac agtttattga ttttatttat tttccttaaa ttttctgaat 600
atatttggtt ctctcattct ttgaattttt cttaatatcc tagattatac atacatccgc 660
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<210> 260
<211> 162
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G353 polypeptide Paralogous to G354

<400> 260

Met Val Ala Ile Ser Glu Ile Lys Ser Thr Val Asp Val Thr Ala Ala
1 5 10 15

Asn Cys Leu Met Leu Leu Ser Arg Val Gly Gln Glu Asn Val Asp Gly
20 25 30

Gly Asp Gln Lys Arg Val Phe Thr Cys Lys Thr Cys Leu Lys Gln Phe
Page 242

35

40

45

His Ser Phe Gln Ala Leu Gly Gly His Arg Ala Ser His Lys Lys Pro
50 55 60

Asn Asn Asp Ala Leu Ser Ser Gly Leu Met Lys Lys Val Lys Thr Ser
65 70 75 80

Ser His Pro Cys Pro Ile Cys Gly Val Glu Phe Pro Met Gly Gln Ala
85 90 95

Leu Gly Gly His Met Arg Arg His Arg Asn Glu Ser Gly Ala Ala Gly
100 105 110

Gly Ala Leu Val Thr Arg Ala Leu Leu Pro Glu Pro Thr Val Thr Thr
115 120 125

Leu Lys Lys Ser Ser Ser Gly Lys Arg Val Ala Cys Leu Asp Leu Ser
130 135 140

Leu Gly Met Val Asp Asn Leu Asn Leu Lys Leu Glu Leu Gly Arg Thr
145 150 155 160

Val Tyr

<210> 261

<211> 1285

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G512; predicted polypeptide sequence is paralogous to G1452

<400> 261

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aaaattcccg gattttactc tttgggcggt ggccgatttc ttacgcgctc tttttgtggc 120

gactgttgta tacgcgcgag ccttcattga cacgaaggcg gttggagttt ctaaggatac 180

ggcggcgctc atggaagcgt cgacggtgtt tcctggggtt aaattctcgc cgacggatgt 240

ggagttgatt tcgtattacc tgaagcggaa gatggatggc ttggagaggt ccgttgaggt 300

tataccggac cttgagattt acaatttcga gccttgggat ttacccgata agtcgattgt 360

gaaatctgat agcgagtggg tcttcttctg tgcgcgtggg aaaaagtatc cacatgggtc 420

acagaacagg agagcaacga agatgggata ctggaaagca actgggaaag agcgtgatgt 480

gaagtctggt tctgaggtca ttggaacaaa gaggacgctt gttttccata ttggtcgtgc 540

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<210> 262

<211> 340

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G512 polypeptide; paralogous to G1452

<400> 262

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Met Asp Thr Lys Ala Val Gly Val Ser Lys Asp Thr Ala Ala Ser Met
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Glu Ala Ser Thr Val Phe Pro Gly Phe Lys Phe Ser Pro Thr Asp Val
          20          25          30

```

```

Glu Leu Ile Ser Tyr Tyr Leu Lys Arg Lys Met Asp Gly Leu Glu Arg
          35          40          45

```

```

Ser Val Glu Val Ile Pro Asp Leu Glu Ile Tyr Asn Phe Glu Pro Trp
          50          55          60

```

```

Asp Leu Pro Asp Lys Ser Ile Val Lys Ser Asp Ser Glu Trp Phe Phe
65          70          75          80

```

```

Phe Cys Ala Arg Gly Lys Lys Tyr Pro His Gly Ser Gln Asn Arg Arg
          85          90          95

```

```

Ala Thr Lys Met Gly Tyr Trp Lys Ala Thr Gly Lys Glu Arg Asp Val
          100         105         110

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Lys Ser Gly Ser Glu Val Ile Gly Thr Lys Arg Thr Leu Val Phe His

115

120

125

Ile Gly Arg Ala Pro Lys Gly Glu Arg Thr Asp Trp Ile Met His Glu
130 135 140

Tyr Cys Val Lys Gly Val Ser Leu Asp Asp Ala Met Val Val Cys Arg
145 150 155 160

Val Arg Arg Asn Lys Glu Tyr Asn Ser Gly Thr Ser Gln Lys Ala Pro
165 170 175

Lys Pro Asn Ser Ser Ala Glu Lys His Ala Lys Val Gln Asn Gly Ala
180 185 190

Thr Ser Ser Gly Ser Pro Ser Asp Trp Asp Asn Leu Val Asp Phe Tyr
195 200 205

Leu Ala Gly Glu Ser Gly Glu Lys Leu Leu Ala Glu Met Ala Glu Ser
210 215 220

Ser Glu Asn Leu Gln Val Asp Asn Asp Glu Asp Phe Phe Ala Asp Ile
225 230 235 240

Leu Arg Asp Glu Ile Ile Asn Leu Asp Glu Ala Val Met Thr Gly Asn
245 250 255

Thr Pro Asn Glu Val Pro Thr Leu Glu Ser Ala Ser Met Glu Ile Arg
260 265 270

Val Leu Pro Leu Pro Asn Met Ile Asp Lys Gln Met Ser Ser Leu Leu
275 280 285

Glu Glu Arg Pro Ser Gln Lys Lys Lys Gly Lys Asp Ala Thr Glu Ser
290 295 300

Leu Ser Ser Cys Phe Val Gly Leu Tyr Ser Ile Lys Ser Val Asn Lys
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Ala Arg Trp Asp Val Ile Ile Gly Val Val Ala Leu Ile Ala Met Leu
325 330 335

Phe Tyr Leu Glu
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<210> 263

<211> 1394

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G596; predicted polypeptide sequence is paralogous to G2789

<400> 263

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<210> 264

<211> 317

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G596 polypeptide; paralogous to G2789

<400> 264

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    20              25              30

Gln Gln Asn His Gly His Asp Ile Asp Gln His Arg Ile Gly Gly Leu
    35              40              45

Lys Arg Asp Arg Asp Ala Asp Ile Asp Pro Asn Glu His Ser Ser Ala
    50              55              60

Gly Lys Asp Gln Ser Thr Pro Gly Ser Gly Gly Glu Ser Gly Gly Gly
    65              70              75              80

Gly Gly Gly Asp Asn His Ile Thr Arg Arg Pro Arg Gly Arg Pro Ala
    85              90              95

Gly Ser Lys Asn Lys Pro Lys Pro Pro Ile Ile Ile Thr Arg Asp Ser
    100             105             110

Ala Asn Ala Leu Lys Ser His Val Met Glu Val Ala Asn Gly Cys Asp
    115             120             125

Val Met Glu Ser Val Thr Val Phe Ala Arg Arg Arg Gln Arg Gly Ile
    130             135             140

Cys Val Leu Ser Gly Asn Gly Ala Val Thr Asn Val Thr Ile Arg Gln
    145             150             155             160

Pro Ala Ser Val Pro Gly Gly Gly Ser Ser Val Val Asn Leu His Gly
    165             170             175

Arg Phe Glu Ile Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala
    180             185             190

Pro Pro Ala Ala Ser Gly Leu Thr Ile Tyr Leu Ala Gly Gly Gln Gly
    195             200             205

Gln Val Val Gly Gly Ser Val Val Gly Pro Leu Met Ala Ser Gly Pro
    210             215             220

Val Val Ile Met Ala Ala Ser Phe Gly Asn Ala Ala Tyr Glu Arg Leu
    225             230             235             240

Pro Leu Glu Glu Asp Asp Gln Glu Glu Gln Thr Ala Gly Ala Val Ala
    245             250             255

Asn Asn Ile Asp Gly Asn Ala Thr Met Gly Gly Gly Thr Gln Thr Gln

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260

265

270

Thr Gln Thr Gln Gln Gln Gln Gln Gln Gln Leu Met Gln Asp Pro Thr
275 280 285

Ser Phe Ile Gln Gly Leu Pro Pro Asn Leu Met Asn Ser Val Gln Leu
290 295 300

Pro Ala Glu Ala Tyr Trp Gly Thr Pro Arg Pro Ser Phe
305 310 315

<210> 265

<211> 925

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G714; predicted polypeptide sequence is paralogous to G489

<400> 265

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ttcagaccat ccagcttacc atcagatcca ccagcaacaa caacaacagc tcaactcaaca      180
gcttcaatct ttctgggaga ctcaattcaa agagattgag aaaaccactg atttcaagaa      240
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<210> 266

<211> 217

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G714 polypeptide; paralogous to G489

<400> 266

Met Asp Gln Gln Gly Gln Ser Ser Ala Met Asn Tyr Gly Ser Asn Pro
1 5 10 15

Tyr Gln Thr Asn Ala Met Thr Thr Thr Pro Thr Gly Ser Asp His Pro
20 25 30

Ala Tyr His Gln Ile His Gln Gln Gln Gln Gln Leu Thr Gln Gln
35 40 45

Leu Gln Ser Phe Trp Glu Thr Gln Phe Lys Glu Ile Glu Lys Thr Thr
50 55 60

Asp Phe Lys Asn His Ser Leu Pro Leu Ala Arg Ile Lys Lys Ile Met
65 70 75 80

Lys Ala Asp Glu Asp Val Arg Met Ile Ser Ala Glu Ala Pro Val Val
85 90 95

Phe Ala Arg Ala Cys Glu Met Phe Ile Leu Glu Leu Thr Leu Arg Ser
100 105 110

Trp Asn His Thr Glu Glu Asn Lys Arg Arg Thr Leu Gln Lys Asn Asp
115 120 125

Ile Ala Ala Ala Val Thr Arg Thr Asp Ile Phe Asp Phe Leu Val Asp
130 135 140

Ile Val Pro Arg Glu Asp Leu Arg Asp Glu Val Leu Gly Gly Val Gly
145 150 155 160

Ala Glu Ala Ala Thr Ala Ala Gly Tyr Pro Tyr Gly Tyr Leu Pro Pro
165 170 175

Gly Thr Ala Pro Ile Gly Asn Pro Gly Met Val Met Gly Asn Pro Gly
180 185 190

Ala Tyr Pro Pro Lys Ala Tyr Met Gly Gln Pro Met Trp Gln Gln Pro
195 200 205

Gly Pro Glu Gln Gln Asp Pro Asp Asn
210 215

<210> 267

<211> 2603

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G877 Predicted polypeptide sequence is paralogous to G175

<400> 267

caaagattag	actaatccga	ctgtgttttt	aatcaatcat	cattttat	aggggagaga	60
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agagaggaag	aaggagaaga	aaaaaatatc	tctttctctc	cggctttcaa	caaaatctct	180
cttttttccct	tcatcagtg	taaattcgga	tccgggtcgg	gtgggttttc	ggtttttggt	240
gttcggatca	gagcacagtt	ggatgtagc	gacggaactg	aggatttcag	tttgcggctg	300
cggcggctgt	gacgggtgtt	gtgtgtcgtc	ttcttttata	aatcaggagt	ttcatcacag	360
tttgatcaga	gattcagcca	aattcttggg	tactaaatgg	ctggttttga	tgaaaatggt	420
gctgtgatgg	gagaatgggt	gcctcgtagt	cctagtcccg	ggacactttt	ctcctctgct	480
attggagaag	agaagagctc	gaaacgtgtt	cttgaaagag	agttatcttt	gaatcatggg	540
caagttattg	gtttagaaga	agacactagt	agtaatcata	acaaggattc	ttcacaaagc	600
aatgtttttc	gaggtgggtc	cagtgaagaa	attgctgcaa	gagctggatt	taatgctcca	660
aggttgaaca	ctgagaatat	ccgcaccaac	accgactttt	ccattgactc	taaccttcga	720
tctccttgct	taaccatctc	ttctcctggc	cttagccctg	caacactctt	ggaatctcct	780
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cctgggtgta	atggtaatgc	attgtcttct	gagaaagcga	aagacgagtt	ctttgatgat	900
attggagcat	cattcagctt	ccatcctgtt	tcaagatcat	cttcctcttt	cttccaaggc	960
acaacagaga	tgatgtcagt	tgattatggg	aactacaaca	atagatcttc	ttctcatcaa	1020
tccgcagaag	aagtaaaacc	tggctctgaa	aacatagaaa	gctccaatct	ttatgggatt	1080
gaaactgaca	atcaaaacgg	gcagaacaag	acatctgatg	tcactacaaa	caccagtctt	1140
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gggtgcgcctg	cagaggatgg	atataactgg	aggaaatacg	gacaaaagtt	ggtcaaagga	1260
agtgagtatc	cgcaagcta	ttacaagtgc	acaaaccgga	attgtcaggt	gaagaagaaa	1320
gttgagagat	caaggggaagg	tcacatcaca	gagattatat	acaaaggagc	tcataatcat	1380
cttaaaccctc	cacctaatcg	ccgctcaggg	atgcaagtag	atggaactga	acaagttgaa	1440
caacaacaac	aacagagaga	ttctgctgca	acgtgggtta	gttgtaataa	cactcaacaa	1500
caaggtggaa	gcaatgagaa	caatgtcgaa	gagggatcta	cgagattcga	gtatggaaac	1560
caatctggat	caattcaagc	tcaaaccgga	ggtcaatacg	agtcaggtga	tcctgtgggt	1620
gtggttgatg	cttcttcaac	attctcta	gatgaagatg	aagatgatcg	agggacacat	1680
ggaagtgttt	ctttgggtta	cgatggagga	ggaggaggtg	ggggaggaga	aggagatgaa	1740
tcagagtcga	aaagaaggaa	actagaagct	tttgcagcag	agatgagtgg	atcaacaaga	1800

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gccatacgtg agccaagagt tggtgtgcag acaacgagtg atggtgacat tcttgatgat 1860
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tattacaaat gcacagctcc aggatgtaca gtgaggaaac atggtgaaag agcttctcat 1980
gatctcaaat ccgttataac aacttacgaa ggcaaacata accatgacgt ccccgctgca 2040
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gcagtttctc accattacca caacggtcat cactcagagc cgccacgtgg gagattcgac 2160
agacaagtca caactaaca tcaagtctct tttagccgct ccttttagctt tcagccacat 2220
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caaccggttg ggatgagtga agcaatgatg cagagagggg tggaacccaa ggttgaaccg 2400
gtttcagatt caggacaatc ggtatataac cagatcatga gtagattacc tcagatttga 2460
aatttactct tcttcttctt cttctgcatt tggtcactcc ttataataac ttttaatttc 2520
tgcttcttct tcttctttca tttattggtt tcaaactttg gggaaggtaa aggctgtttt 2580
attgttaaaa aaaaaaaaaa aaa 2603

```

<210> 268

<211> 687

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G877 polypeptide Paralogous to G175

<400> 268

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Met Ala Gly Phe Asp Glu Asn Val Ala Val Met Gly Glu Trp Val Pro
1           5           10          15

```

```

Arg Ser Pro Ser Pro Gly Thr Leu Phe Ser Ser Ala Ile Gly Glu Glu
          20          25          30

```

```

Lys Ser Ser Lys Arg Val Leu Glu Arg Glu Leu Ser Leu Asn His Gly
          35          40          45

```

```

Gln Val Ile Gly Leu Glu Glu Asp Thr Ser Ser Asn His Asn Lys Asp
          50          55          60

```

```

Ser Ser Gln Ser Asn Val Phe Arg Gly Gly Leu Ser Glu Arg Ile Ala
65          70          75          80

```

```

Ala Arg Ala Gly Phe Asn Ala Pro Arg Leu Asn Thr Glu Asn Ile Arg
          85          90          95

```

```

Thr Asn Thr Asp Phe Ser Ile Asp Ser Asn Leu Arg Ser Pro Cys Leu

```

100

105

110

Thr Ile Ser Ser Pro Gly Leu Ser Pro Ala Thr Leu Leu Glu Ser Pro
 115 120 125

Val Phe Leu Ser Asn Pro Leu Ala Gln Pro Ser Pro Thr Thr Gly Lys
 130 135 140

Phe Pro Phe Leu Pro Gly Val Asn Gly Asn Ala Leu Ser Ser Glu Lys
 145 150 155 160

Ala Lys Asp Glu Phe Phe Asp Asp Ile Gly Ala Ser Phe Ser Phe His
 165 170 175

Pro Val Ser Arg Ser Ser Ser Ser Phe Phe Gln Gly Thr Thr Glu Met
 180 185 190

Met Ser Val Asp Tyr Gly Asn Tyr Asn Asn Arg Ser Ser Ser His Gln
 195 200 205

Ser Ala Glu Glu Val Lys Pro Gly Ser Glu Asn Ile Glu Ser Ser Asn
 210 215 220

Leu Tyr Gly Ile Glu Thr Asp Asn Gln Asn Gly Gln Asn Lys Thr Ser
 225 230 235 240

Asp Val Thr Thr Asn Thr Ser Leu Glu Thr Val Asp His Gln Glu Glu
 245 250 255

Glu Glu Glu Gln Arg Arg Gly Asp Ser Met Ala Gly Gly Ala Pro Ala
 260 265 270

Glu Asp Gly Tyr Asn Trp Arg Lys Tyr Gly Gln Lys Leu Val Lys Gly
 275 280 285

Ser Glu Tyr Pro Arg Ser Tyr Tyr Lys Cys Thr Asn Pro Asn Cys Gln
 290 295 300

Val Lys Lys Lys Val Glu Arg Ser Arg Glu Gly His Ile Thr Glu Ile
 305 310 315 320

Ile Tyr Lys Gly Ala His Asn His Leu Lys Pro Pro Pro Asn Arg Arg
 325 330 335

Ser Gly Met Gln Val Asp Gly Thr Glu Gln Val Glu Gln Gln Gln Gln
 340 345 350

Gln Arg Asp Ser Ala Ala Thr Trp Val Ser Cys Asn Asn Thr Gln Gln

355

360

365

Gln Gly Gly Ser Asn Glu Asn Asn Val Glu Glu Gly Ser Thr Arg Phe
370 375 380

Glu Tyr Gly Asn Gln Ser Gly Ser Ile Gln Ala Gln Thr Gly Gly Gln
385 390 395 400

Tyr Glu Ser Gly Asp Pro Val Val Val Val Asp Ala Ser Ser Thr Phe
405 410 415

Ser Asn Asp Glu Asp Glu Asp Asp Arg Gly Thr His Gly Ser Val Ser
420 425 430

Leu Gly Tyr Asp Gly Gly Gly Gly Gly Gly Gly Glu Gly Asp Glu
435 440 445

Ser Glu Ser Lys Arg Arg Lys Leu Glu Ala Phe Ala Ala Glu Met Ser
450 455 460

Gly Ser Thr Arg Ala Ile Arg Glu Pro Arg Val Val Val Gln Thr Thr
465 470 475 480

Ser Asp Val Asp Ile Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly
485 490 495

Gln Lys Val Val Lys Gly Asn Pro Asn Pro Arg Ser Tyr Tyr Lys Cys
500 505 510

Thr Ala Pro Gly Cys Thr Val Arg Lys His Val Glu Arg Ala Ser His
515 520 525

Asp Leu Lys Ser Val Ile Thr Thr Tyr Glu Gly Lys His Asn His Asp
530 535 540

Val Pro Ala Ala Arg Asn Ser Ser His Gly Gly Gly Gly Asp Ser Gly
545 550 555 560

Asn Gly Asn Ser Gly Gly Ser Ala Ala Val Ser His His Tyr His Asn
565 570 575

Gly His His Ser Glu Pro Pro Arg Gly Arg Phe Asp Arg Gln Val Thr
580 585 590

Thr Asn Asn Gln Ser Pro Phe Ser Arg Pro Phe Ser Phe Gln Pro His
595 600 605

Leu Gly Pro Pro Ser Gly Phe Ser Phe Gly Leu Gly Gln Thr Gly Leu

610

615

620

Val Asn Leu Ser Met Pro Gly Leu Ala Tyr Gly Gln Gly Lys Met Pro
625 630 635 640

Gly Leu Pro His Pro Tyr Met Thr Gln Pro Val Gly Met Ser Glu Ala
645 650 655

Met Met Gln Arg Gly Met Glu Pro Lys Val Glu Pro Val Ser Asp Ser
660 665 670

Gly Gln Ser Val Tyr Asn Gln Ile Met Ser Arg Leu Pro Gln Ile
675 680 685

<210> 269

<211> 1008

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G1357; predicted polypeptide sequence is paralogous to G1452

<400> 269

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agatctgttg agattatacc tgaggttgag atttacaact tcgagccttg ggatttacct      180
gataagtcta tcgttaaadc ggatagcgaa tggttcttct tctgtgctcg cggtagaag      240
tatccccacg gttcacagaa cagaagagca accaagatag gatattggaa agccacagga      300
aaagagcgta atgtgaagtc aggttctgag gtcattggaa caaagagaac gcttgtattc      360
cacattggcc gcgcgcaaaa aggaggaaga acggaatggc ttatgcatga gtactgcatg      420
attggagtat cactggatgc tctggttatt tgccgactta ggaggaatac tgaatttcaa      480
gggagtacaa ttcaaaagcc accacaacca agtttaccac tggataagca cgtaaacttg      540
cggaatgaag ctatttcaga aagtatttat ggttgggaaa ctatggttga tttctactta      600
tcaagtgagt cagggcaaga actacttagt gaaatagcag aatcttcaca atcttcacaa      660
aatccacagg ttcctagtga agaagatttc tatgccgata tactgaggga tgaaatagta      720
aagctagatg atccggcggc atccggtaat aactgatca atgtaccaag gcttcaaaca      780
gagtccaata ccacaagagt actaccttta cctgacatgg tagacaaaca aatgcaatcg      840
ttgctacaga aactaccatt aaaaatgac actggagaag agaacaacat atccatgtca      900
aattgcttta tcggtatcta ctgattaag tctataaacc gagcgcgatg ggacgttggt      960
gtttggttac tcgttatgat agccgtgttg gtgttttatt tagtgtga      1008
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<210> 270

<211> 335

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G1357 polypeptide; paralogous to G1452

<400> 270

Met Ala Ala Ala Pro Pro Ile Glu Pro Ala Val Thr Thr Thr Phe Pro
1 5 10 15

Gly Phe Lys Phe Ser Pro Thr Asp Ile Glu Leu Ile Ser Tyr Tyr Leu
20 25 30

Lys Arg Lys Met Asp Gly Leu Glu Arg Ser Val Glu Ile Ile Pro Glu
35 40 45

Val Glu Ile Tyr Asn Phe Glu Pro Trp Asp Leu Pro Asp Lys Ser Ile
50 55 60

Val Lys Ser Asp Ser Glu Trp Phe Phe Phe Cys Ala Arg Gly Lys Lys
65 70 75 80

Tyr Pro His Gly Ser Gln Asn Arg Arg Ala Thr Lys Ile Gly Tyr Trp
85 90 95

Lys Ala Thr Gly Lys Glu Arg Asn Val Lys Ser Gly Ser Glu Val Ile
100 105 110

Gly Thr Lys Arg Thr Leu Val Phe His Ile Gly Arg Ala Pro Lys Gly
115 120 125

Gly Arg Thr Glu Trp Leu Met His Glu Tyr Cys Met Ile Gly Val Ser
130 135 140

Leu Asp Ala Leu Val Ile Cys Arg Leu Arg Arg Asn Thr Glu Phe Gln
145 150 155 160

Gly Ser Thr Ile Gln Lys Pro Pro Gln Pro Ser Leu Pro Leu Asp Lys
165 170 175

His Val Asn Leu Arg Asn Glu Ala Ile Ser Glu Ser Ile Tyr Gly Trp
180 185 190

Glu Thr Met Val Asp Phe Tyr Leu Ser Ser Glu Ser Gly Gln Glu Leu
195 200 205

Leu Ser Glu Ile Ala Glu Ser Ser Gln Ser Ser Gln Asn Pro Gln Val
210 215 220

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Pro Ser Glu Glu Asp Phe Tyr Ala Asp Ile Leu Arg Asp Glu Ile Val
225 230 235 240

Lys Leu Asp Asp Pro Ala Val Ser Gly Asn Thr Leu Ile Asn Val Pro
245 250 255

Arg Leu Gln Thr Glu Ser Asn Thr Thr Arg Val Leu Pro Leu Pro Asp
260 265 270

Met Val Asp Lys Gln Met Gln Ser Leu Leu Gln Lys Leu Pro Leu Gln
275 280 285

Asn Asp Thr Gly Glu Glu Asn Asn Ile Ser Met Ser Asn Cys Phe Ile
290 295 300

Gly Ile Tyr Ser Ile Lys Ser Ile Asn Arg Ala Arg Trp Asp Val Val
305 310 315 320

Val Trp Leu Leu Val Met Ile Ala Val Leu Val Phe Tyr Leu Val
325 330 335

<210> 271

<211> 844

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G1387 Predicted polypeptide sequence is paralogous to G975

<400> 271

tctctctccc actctcactt tctctcctat tcttagttcg tgtcagaaac acacagagaa	60
attaagaacc ctaatttaaa acagaagaat ggtacattcg aagaagttcc gaggtgtccg	120
ccagcgtcag tggggttctt gggtttctga gattcgtcat cctctcttga agagaagagt	180
gtggctagga acattcgaca cggcggaac agcggctaga gcctacgacc aagccgcggt	240
tctaataaac ggccagagcg cgaagactaa cttccccgct atcaaatcga acggttcaaa	300
ttccttgagg attaatcttg cgttaaggct tcccaaatca ttatcggaac tattgaacgc	360
taagctaagg aagaactgta aagaccagac accgtatctg acgtgtctcc gcctcgacaa	420
cgacagctca cacatcggcg tctggcagaa acgcgcgggg tcaaaaacga gtccaaactg	480
ggtcaagctt gttgaactag gtgacaaagt taacgcacgt cccggtggtg atattgagac	540
taataagatg aaggtagcaa acgaagacgt tcaggaagat gatcaaatgg cgatgcagat	600
gatcgaggag ttgcttaact ggacctgtcc tggatctgga tccattgcac aggtctaaag	660
gagaatcatt gaattatatg atcaagataa taatatagtt gaggggttaat aataatcgag	720
ggtaagtaat ttacgtgtag ctaataatta atataatttt cgaacatata tatgaatata	780

tgatagctct agaaatgagt acgtatatat acgtaaacad ttttcctcaa atatagtata 840
tgtg 844

<210> 272
<211> 189
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G1387 polypeptide Paralogous to G975

<400> 272

Met Val His Ser Lys Lys Phe Arg Gly Val Arg Gln Arg Gln Trp Gly
1 5 10 15

Ser Trp Val Ser Glu Ile Arg His Pro Leu Leu Lys Arg Arg Val Trp
20 25 30

Leu Gly Thr Phe Asp Thr Ala Glu Thr Ala Ala Arg Ala Tyr Asp Gln
35 40 45

Ala Ala Val Leu Met Asn Gly Gln Ser Ala Lys Thr Asn Phe Pro Val
50 55 60

Ile Lys Ser Asn Gly Ser Asn Ser Leu Glu Ile Asn Ser Ala Leu Arg
65 70 75 80

Ser Pro Lys Ser Leu Ser Glu Leu Leu Asn Ala Lys Leu Arg Lys Asn
85 90 95

Cys Lys Asp Gln Thr Pro Tyr Leu Thr Cys Leu Arg Leu Asp Asn Asp
100 105 110

Ser Ser His Ile Gly Val Trp Gln Lys Arg Ala Gly Ser Lys Thr Ser
115 120 125

Pro Asn Trp Val Lys Leu Val Glu Leu Gly Asp Lys Val Asn Ala Arg
130 135 140

Pro Gly Gly Asp Ile Glu Thr Asn Lys Met Lys Val Arg Asn Glu Asp
145 150 155 160

Val Gln Glu Asp Asp Gln Met Ala Met Gln Met Ile Glu Glu Leu Leu
165 170 175

Asn Trp Thr Cys Pro Gly Ser Gly Ser Ile Ala Gln Val
180 185

<210> 273

<211> 896
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G1634; predicted polypeptide sequence is paralogous to G2701

<400> 273
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tctgaccacc ggtttgtagt tcaagagatg atgtgcttgc aaagctcgag ctggactaaa 120
gaagagaaca agaagtttga gcgagctctt gctgtctacg ctgatgacac gcctgatcgc 180
tggttcaaag ttgctgctat gatccctgga aagaccatat cagatgtcat gaggcaatac 240
tctaagcttg aagaagacct cttcgatata gaagcaggac ttgtcccgat cccgggttac 300
cgttcagtta ctcttctgtg atttgatcag gttgtgagtc cacgtgactt tgatgcgtat 360
cgtaaacttc ctaatggagc cagaggattt gatcaagacc gtaggaaagg agttccatgg 420
acggaggaag aacacaggag attcttggtta gggcttctca agtatgggaa aggagattgg 480
agaaacatat cgaggaactt tgtgggatca aaaacaccaa ctgaggttgc aagtcatgcc 540
caaaagtact accaaagaca gctttccggt gcgaaagaca aacgacggcc tagcattcac 600
gacatcacca ccgtcaatct tctcaatgcc aatcttagcc gtccatcgtc tgatcacggc 660
tgcttagtct caaaacaggc cgagccgaaa ctagggttca ccgacaggga taatgcagag 720
gagggagtta tgtttcttgg tcagaatcta tcctcggtct tctcttccta cgatcctgcc 780
attaagtttt ccggagcaaa tgtttacggg gaaggaggtt actgtatctc acaagatctt 840
gaaacgagaa aatgagaatt ttgaaatatt aactattgca acgaaaccat aattgc 896

<210> 274
<211> 277
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G1634 polypeptide; paralogous to G2701

<400> 274

Met Glu Thr Leu His Pro Leu Leu Ser His Val Pro Thr Ser Asp His
1 5 10 15

Arg Phe Val Val Gln Glu Met Met Cys Leu Gln Ser Ser Ser Trp Thr
20 25 30

Lys Glu Glu Asn Lys Lys Phe Glu Arg Ala Leu Ala Val Tyr Ala Asp
35 40 45

Asp Thr Pro Asp Arg Trp Phe Lys Val Ala Ala Met Ile Pro Gly Lys
50 55 60

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Thr Ile Ser Asp Val Met Arg Gln Tyr Ser Lys Leu Glu Glu Asp Leu
65 70 75 80

Phe Asp Ile Glu Ala Gly Leu Val Pro Ile Pro Gly Tyr Arg Ser Val
85 90 95

Thr Pro Cys Gly Phe Asp Gln Val Val Ser Pro Arg Asp Phe Asp Ala
100 105 110

Tyr Arg Lys Leu Pro Asn Gly Ala Arg Gly Phe Asp Gln Asp Arg Arg
115 120 125

Lys Gly Val Pro Trp Thr Glu Glu Glu His Arg Arg Phe Leu Leu Gly
130 135 140

Leu Leu Lys Tyr Gly Lys Gly Asp Trp Arg Asn Ile Ser Arg Asn Phe
145 150 155 160

Val Gly Ser Lys Thr Pro Thr Gln Val Ala Ser His Ala Gln Lys Tyr
165 170 175

Tyr Gln Arg Gln Leu Ser Gly Ala Lys Asp Lys Arg Arg Pro Ser Ile
180 185 190

His Asp Ile Thr Thr Val Asn Leu Leu Asn Ala Asn Leu Ser Arg Pro
195 200 205

Ser Ser Asp His Gly Cys Leu Val Ser Lys Gln Ala Glu Pro Lys Leu
210 215 220

Gly Phe Thr Asp Arg Asp Asn Ala Glu Glu Gly Val Met Phe Leu Gly
225 230 235 240

Gln Asn Leu Ser Ser Val Phe Ser Ser Tyr Asp Pro Ala Ile Lys Phe
245 250 255

Ser Gly Ala Asn Val Tyr Gly Glu Gly Gly Tyr Cys Ile Ser Gln Asp
260 265 270

Leu Glu Thr Arg Lys
275

<210> 275

<211> 625

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G1889 Predicted polypeptide sequence is paralogous to G354

```

<400> 275
acacgatcaa aactcattat tcaacaaagt cttcgtttca tttttcattt ttcattttctc      60
aaccaaaaaa aaaaagagtg attttttttt taatcatcag tcaaattggaa aggggaagat      120
cagatatgga gatgataaac aacatggcaa attgcttgat tcttctatca aaggcccatc      180
aaaacgacac caaaagccgt gttttcgcgt gcaagacatg caacaaagag ttcccgcgtc      240
tccaagcctt gggagggtcac cgagccagcc accggcgatc cgcagcgctt gaaggccacg      300
cacctccttc tcctaagaga gtcaaaccgg tgaaacacga gtgtcccata tgtggtgctg      360
agttcgcggt agggcaggcc ttaggtggtc acatgaggaa gcatagaggt ggatcaggag      420
gaggaggtgg ccggagtttg gcgccggcta cagcgccggt gacgatgaag aaatcaggcg      480
gtggtaatgg aaaaagagtt ttgtgttttg acttgaactt gacgccttta gagaacgaag      540
atgtgaagtt ggagcttggg aggtttatct tctgattttt gttcgttttt ctttttaggg      600
tataacttggt tagggtaagt ttatt                                           625

```

```

<210> 276
<211> 156
<212> PRT
<213> Arabidopsis thaliana

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```

<220>
<223> G1889 polypeptide Paralogous to G354

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```

<400> 276

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```

Met Glu Arg Gly Arg Ser Asp Met Glu Met Ile Asn Asn Met Ala Asn
1           5           10           15

```

```

Cys Leu Ile Leu Leu Ser Lys Ala His Gln Asn Asp Thr Lys Ser Arg
          20           25           30

```

```

Val Phe Ala Cys Lys Thr Cys Asn Lys Glu Phe Pro Ser Phe Gln Ala
          35           40           45

```

```

Leu Gly Gly His Arg Ala Ser His Arg Arg Ser Ala Ala Leu Glu Gly
          50           55           60

```

```

His Ala Pro Pro Ser Pro Lys Arg Val Lys Pro Val Lys His Glu Cys
65           70           75           80

```

```

Pro Ile Cys Gly Ala Glu Phe Ala Val Gly Gln Ala Leu Gly Gly His
          85           90           95

```

```

Met Arg Lys His Arg Gly Gly Ser Gly Gly Gly Gly Gly Arg Ser Leu
          100          105          110

```

```

Ala Pro Ala Thr Ala Pro Val Thr Met Lys Lys Ser Gly Gly Gly Asn

```


Gly Lys Arg Val Leu Cys Leu Asp Leu Asn Leu Thr Pro Leu Glu Asn
130 135 140

Glu Asp Leu Lys Leu Glu Leu Gly Arg Phe Ile Phe
145 150 155

<210> 277

<211> 1323

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G1940; predicted polypeptide sequence is paralogous to G2854

<400> 277

tcgactttgt cgcgcgtagt gatgcagcaa ccaccgtcaa acgccgccgg agctggacag	60
ataccatcag gacaacagca tttgtggatg atgatgcaac agcagcagca gcagcagcag	120
atgcagttgt ctgcggcgcc actaggtcaa catcagtagc gtattggatc tcagaatcca	180
ggatccgcta gcgatgttaa gtcgttgtgg atcggagact tgcagcaatg gatggacgag	240
aactacatca tgagcgtctt tgctcagtct ggcgaggcta catcagctaa agtcattcgt	300
aataagctga cgggacaatc tgaagggttat ggattcattg agttcgtcag ccactctgta	360
gcagagcggg ttttgcagac ttacaatggg gctcccatgc cgagcactga acagacgttt	420
aggctcaact gggctcaggc tggggctgga gagaaacgat tccagactga agggcctgac	480
cataccattt tcgtaggtga cttggcacct gaggtgactg actatatgct ctcggacaca	540
ttcaagaatg tgtatgggtc tgtcaaaggg gctaaagttg tgcttgacag gaccactgga	600
aggccaagg ggtatgggtt tgtaggggtt gcggatgaaa atgagcagat gcgtgccatg	660
actgaaatga atgggtcaata ctgctcgaca aggcctatgc gtattgggtc ggctgccaat	720
aagaatgctc ttccgatgca accagctatg tatcaaaaca ctcaaggagc aaatgctgga	780
gataatgata ctaataacac aacaattttt gttggagggtc tggatgctaa tggtacagac	840
gatgaattaa agtcaatttt tgggtcaattt ggtgaacttc ttcatgtgaa aatacctcca	900
ggaaaacgtt gtggattcgt tcaatatgcc aacaaggcgt ctgcagagca tgcactttcg	960
gtgctgaatg gaacacaatt aggtggacaa agcatccgtc tttcgtgggg acgtagtcca	1020
aacaagcagt ctgatcaagc gcaatggaac ggtggtggat actatggata ccctccacag	1080
ccacagggcg gctatggtta tgcagctcaa ccaccaactc aagaccctaa tgcgtactat	1140
ggtggttaca ctggctatgg caactatcag cagcaacgtc agtgaaacat caacatcagc	1200
tatttctacc aatgtcttgg aacaaaagat gagcgattgt gtcttattag gacttctaga	1260
ttaaaagtgc tctctttttg tttgagtttt attttgcaaa tgagtcgatc ttgaatttgc	1320

tat

1323

<210> 278

<211> 387

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G1940 polypeptide; paralogous to G2854

<400> 278

Met Gln Gln Pro Pro Ser Asn Ala Ala Gly Ala Gly Gln Ile Pro Ser
 1 5 10 15

Gly Gln Gln His Leu Trp Met Met Met Gln Gln Gln Gln Gln Gln Gln
 20 25 30

Gln Met Gln Leu Ser Ala Ala Pro Leu Gly Gln His Gln Tyr Gly Ile
 35 40 45

Gly Ser Gln Asn Pro Gly Ser Ala Ser Asp Val Lys Ser Leu Trp Ile
 50 55 60

Gly Asp Leu Gln Gln Trp Met Asp Glu Asn Tyr Ile Met Ser Val Phe
 65 70 75 80

Ala Gln Ser Gly Glu Ala Thr Ser Ala Lys Val Ile Arg Asn Lys Leu
 85 90 95

Thr Gly Gln Ser Glu Gly Tyr Gly Phe Ile Glu Phe Val Ser His Ser
 100 105 110

Val Ala Glu Arg Val Leu Gln Thr Tyr Asn Gly Ala Pro Met Pro Ser
 115 120 125

Thr Glu Gln Thr Phe Arg Leu Asn Trp Ala Gln Ala Gly Ala Gly Glu
 130 135 140

Lys Arg Phe Gln Thr Glu Gly Pro Asp His Thr Ile Phe Val Gly Asp
 145 150 155 160

Leu Ala Pro Glu Val Thr Asp Tyr Met Leu Ser Asp Thr Phe Lys Asn
 165 170 175

Val Tyr Gly Ser Val Lys Gly Ala Lys Val Val Leu Asp Arg Thr Thr
 180 185 190

Gly Arg Ser Lys Gly Tyr Gly Phe Val Arg Val Ala Asp Glu Asn Glu
 195 200 205

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Gln Met Arg Ala Met Thr Glu Met Asn Gly Gln Tyr Cys Ser Thr Arg
210 215 220

Pro Met Arg Ile Gly Pro Ala Ala Asn Lys Asn Ala Leu Pro Met Gln
225 230 235 240

Pro Ala Met Tyr Gln Asn Thr Gln Gly Ala Asn Ala Gly Asp Asn Asp
245 250 255

Pro Asn Asn Thr Thr Ile Phe Val Gly Gly Leu Asp Ala Asn Val Thr
260 265 270

Asp Asp Glu Leu Lys Ser Ile Phe Gly Gln Phe Gly Glu Leu Leu His
275 280 285

Val Lys Ile Pro Pro Gly Lys Arg Cys Gly Phe Val Gln Tyr Ala Asn
290 295 300

Lys Ala Ser Ala Glu His Ala Leu Ser Val Leu Asn Gly Thr Gln Leu
305 310 315 320

Gly Gly Gln Ser Ile Arg Leu Ser Trp Gly Arg Ser Pro Asn Lys Gln
325 330 335

Ser Asp Gln Ala Gln Trp Asn Gly Gly Gly Tyr Tyr Gly Tyr Pro Pro
340 345 350

Gln Pro Gln Gly Gly Tyr Gly Tyr Ala Ala Gln Pro Pro Thr Gln Asp
355 360 365

Pro Asn Ala Tyr Tyr Gly Gly Tyr Thr Gly Tyr Gly Asn Tyr Gln Gln
370 375 380

Gln Arg Gln
385

<210> 279
<211> 513
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G1974 Predicted polypeptide sequence is paralogous to G354

<400> 279
atggttgctg aaagtgataa tcgtgatctg acggtggata cggcggcgag ctgtctgatg 60
ttgttatcag gaattggaga acacgacgga agaaagaaac gtgttttccg atgcaagact 120
tgtgagagag acttcgattc gttccaagct ttaggaggcc accgtgcaag cactcgaaa 180

MBI0058CIP.ST25.txt

ctaaccaaca gtgacgataa atcacttcct ggatcaccaa agaagaagcc taaaactacg 240
 actacgacga cggctcatac ttgtccgatt tgtggcttg agtttccgat gggacaagct 300
 cttggtgggtc acatgaggaa acataggaac gagaaagaac gagaaaaggc ttctaacgta 360
 ttggttacgc attctttcat gccggagacg acaacggtga cgactttgaa gaaatcgagt 420
 agtgggaaga gaggggcgtg tttggatttc gacttaactt cggtgagag ctttgtcaac 480
 acggaattgg agttgggaag aacgatgtac tga 513

<210> 280

<211> 170

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G1974 polypeptide Paralogous to G354

<400> 280

Met Val Ala Glu Ser Asp Asn Arg Asp Leu Thr Val Asp Thr Ala Ala
 1 5 10 15

Ser Cys Leu Met Leu Leu Ser Gly Ile Gly Glu His Asp Gly Arg Lys
 20 25 30

Lys Arg Val Phe Arg Cys Lys Thr Cys Glu Arg Asp Phe Asp Ser Phe
 35 40 45

Gln Ala Leu Gly Gly His Arg Ala Ser His Ser Lys Leu Thr Asn Ser
 50 55 60

Asp Asp Lys Ser Leu Pro Gly Ser Pro Lys Lys Lys Pro Lys Thr Thr
 65 70 75 80

Thr Thr Thr Thr Ala His Thr Cys Pro Ile Cys Gly Leu Glu Phe Pro
 85 90 95

Met Gly Gln Ala Leu Gly Gly His Met Arg Lys His Arg Asn Glu Lys
 100 105 110

Glu Arg Glu Lys Ala Ser Asn Val Leu Val Thr His Ser Phe Met Pro
 115 120 125

Glu Thr Thr Thr Val Thr Thr Leu Lys Lys Ser Ser Ser Gly Lys Arg
 130 135 140

Val Ala Cys Leu Asp Phe Asp Leu Thr Ser Val Glu Ser Phe Val Asn
 145 150 155 160

Thr Glu Leu Glu Leu Gly Arg Thr Met Tyr

<210> 281
 <211> 1383
 <212> DNA
 <213> Arabidopsis thaliana

<220>

<223> G2153 Predicted polypeptide sequence is paralogous to G1073

<400> 281

ttcttgctta gtatcattct ttgtcgtggt cttttaatta accttttgca atttgtcttg	60
tgttttctcac aacacaaaaa cttgtaaaag tgttaaaaaa tcaagatctg aaaaatctta	120
tcaccgcttc taggtttttc agtttttttt cttccttttc ctgatctaaa ttaacttata	180
tttcttaggg tttcacttct tgaaacattt aatcagaatt aattaacctc tctagggctt	240
tcatggcgaa tccatggtgg acaggacaag tgaacctatc cggcctcgaa acgacgccgc	300
ctggttcctc tcagttaaag aaaccagatc tccacatctc catgaacatg gccatggact	360
caggtcacaa taatcatcac catcaccaag aagtcgataa caacaacaac gacgacgata	420
gagacaactt gagtggagac gaccacgagc cacgtgaagg agccgtagaa gccccacgc	480
gccgtccacg tggacgtcct gctggttcca agaacaaacc aaagccaccg atcttcgtca	540
ctcgcgattc tccaaatgct ctcaagagcc atgtcatgga gatcgctagt gggactgacg	600
tcatcgaaac cctagctact tttgctaggc ggcgtcaacg tggcatctgc atcttgagcg	660
gaaatggcac agtggctaac gtcaccctcc gtcaaccctc gaccgctgcc gttgcggcgg	720
ctcctgggtg tgccgctggt ttggctttac aagggagggt tgagattctt tctttaaccg	780
gttctttctt gccaggaccg gctccacctg gttccaccgg tttaacgatt tacttagccg	840
gtggtcaagg tcaggttggt ggaggaagcg tgggtggccc attgatggca gcaggcccg	900
tgatgctgat cgccgccacg ttctctaacg cgacttacga gagattgcca ttggaggagg	960
aagaggcagc agagagaggc ggtggtggag gcagcggagg agtggttccg gggcagctcg	1020
gaggcggagg ttcgccacta agcagcgggt ctggtggagg cgacggtaac caaggacttc	1080
cggtgtataa tatgccggga aatcttgttt ctaatggtgg cagtggtgga ggaggacaga	1140
tgagcggcca agaagcttat gggtgggctc aagctagggtc aggattttta cgtgcgttaa	1200
aatggttttt aatttacaga agttaacaat aagattataa tgatgtttat tatgatgatg	1260
aaaaccagtc agttgctact tggtactagt gagctatata gtttgtggac attatattat	1320
gttctctctt gactatgatt attatttgct aaatttcact tagctaaaaa aaaaaaaaaa	1380
aaa	1383

<210> 282
 <211> 315
 <212> PRT

<213> Arabidopsis thaliana

<220>

<223> G2153 polypeptide Paralogous to G1073

<400> 282

Met Ala Asn Pro Trp Trp Thr Gly Gln Val Asn Leu Ser Gly Leu Glu
1 5 10 15

Thr Thr Pro Pro Gly Ser Ser Gln Leu Lys Lys Pro Asp Leu His Ile
20 25 30

Ser Met Asn Met Ala Met Asp Ser Gly His Asn Asn His His His His
35 40 45

Gln Glu Val Asp Asn Asn Asn Asn Asp Asp Asp Arg Asp Asn Leu Ser
50 55 60

Gly Asp Asp His Glu Pro Arg Glu Gly Ala Val Glu Ala Pro Thr Arg
65 70 75 80

Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys Asn Lys Pro Lys Pro Pro
85 90 95

Ile Phe Val Thr Arg Asp Ser Pro Asn Ala Leu Lys Ser His Val Met
100 105 110

Glu Ile Ala Ser Gly Thr Asp Val Ile Glu Thr Leu Ala Thr Phe Ala
115 120 125

Arg Arg Arg Gln Arg Gly Ile Cys Ile Leu Ser Gly Asn Gly Thr Val
130 135 140

Ala Asn Val Thr Leu Arg Gln Pro Ser Thr Ala Ala Val Ala Ala Ala
145 150 155 160

Pro Gly Gly Ala Ala Val Leu Ala Leu Gln Gly Arg Phe Glu Ile Leu
165 170 175

Ser Leu Thr Gly Ser Phe Leu Pro Gly Pro Ala Pro Pro Gly Ser Thr
180 185 190

Gly Leu Thr Ile Tyr Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly
195 200 205

Ser Val Val Gly Pro Leu Met Ala Ala Gly Pro Val Met Leu Ile Ala
210 215 220

Ala Thr Phe Ser Asn Ala Thr Tyr Glu Arg Leu Pro Leu Glu Glu Glu

225 230 235 240

Glu Ala Ala Glu Arg Gly Gly Gly Gly Gly Ser Gly Gly Val Val Pro
245 250 255

Gly Gln Leu Gly Gly Gly Gly Ser Pro Leu Ser Ser Gly Ala Gly Gly
260 265 270

Gly Asp Gly Asn Gln Gly Leu Pro Val Tyr Asn Met Pro Gly Asn Leu
275 280 285

Val Ser Asn Gly Gly Ser Gly Gly Gly Gly Gln Met Ser Gly Gln Glu
290 295 300

Ala Tyr Gly Trp Ala Gln Ala Arg Ser Gly Phe
305 310 315

<210> 283
<211> 653
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G2583 Predicted polypeptide sequence is paralogous to G975

<400> 283
caaatacagaa aatataagagt ttgaaggaaa ctaaaagatg gtacattcga ggaagttccg 60
aggtgtccgc cagcgacaat ggggttcttg ggtctctgag attcgccatc ctctattgaa 120
gagaagagtg tggcttgga ctttcgaaac ggcagaagcg gctgcaagag catacgacca 180
agcggctctt ctaatagaacg gccaaaacgc taagaccaat ttccctgtcg taaaatcaga 240
ggaaggctcc gatcacgta aagatgttaa ctctccgttg atgtcaccaa agtcattatc 300
tgagcttttg aacgctaagc taaggaagag ctgcaaagac ctaacgcctt ctttgacgtg 360
tctccgtctt gatactgaca gttcccat tggagtttg cagaaacggg ccgggtcgaa 420
aacaagtccg acttgggtca tgcgcctcga acttggaac gtagtcaacg aaagtgcggt 480
tgacttaggg ttgactacga tgaacaaaca aaacgttgag aaagaagaag aagaagaaga 540
agctattatt agtgatgagg atcagttagc tatggagatg atcgaggagt tgctgaattg 600
gagttgactt ttgacttta cttgttgcaa gtccacaagg ggtaagggtt ttc 653

<210> 284
<211> 189
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G2583 polypeptide Paralogous to G975

<400> 284

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Met Val His Ser Arg Lys Phe Arg Gly Val Arg Gln Arg Gln Trp Gly
1 5 10 15

Ser Trp Val Ser Glu Ile Arg His Pro Leu Leu Lys Arg Arg Val Trp
20 25 30

Leu Gly Thr Phe Glu Thr Ala Glu Ala Ala Ala Arg Ala Tyr Asp Gln
35 40 45

Ala Ala Leu Leu Met Asn Gly Gln Asn Ala Lys Thr Asn Phe Pro Val
50 55 60

Val Lys Ser Glu Glu Gly Ser Asp His Val Lys Asp Val Asn Ser Pro
65 70 75 80

Leu Met Ser Pro Lys Ser Leu Ser Glu Leu Leu Asn Ala Lys Leu Arg
85 90 95

Lys Ser Cys Lys Asp Leu Thr Pro Ser Leu Thr Cys Leu Arg Leu Asp
100 105 110

Thr Asp Ser Ser His Ile Gly Val Trp Gln Lys Arg Ala Gly Ser Lys
115 120 125

Thr Ser Pro Thr Trp Val Met Arg Leu Glu Leu Gly Asn Val Val Asn
130 135 140

Glu Ser Ala Val Asp Leu Gly Leu Thr Thr Met Asn Lys Gln Asn Val
145 150 155 160

Glu Lys Glu Glu Glu Glu Glu Glu Ala Ile Ile Ser Asp Glu Asp Gln
165 170 175

Leu Ala Met Glu Met Ile Glu Glu Leu Leu Asn Trp Ser
180 185

<210> 285

<211> 341

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G682; Predicted polypeptide sequence is paralogous to G226

<400> 285

acatggataa ccatcgcagg actaagcaac ccaagaccaa ctccatcggtt acttcttctt 60

ctgaaggaac agaagtgagt agtcttgagt gggaagttgt gaacatgagt caagaagaag 120

aagatttggt ctctcgaatg cataagcttg tcggtgacag gtgggaactg atagctggga 180

MBI0058CIP.ST25.txt

```

ggatcccagg aagaaccgct ggagaaattg agaggttttg ggtcatgaaa aattgaaaag      240
tgatcaatat atctctatag tttcactgat tgtttcgatt atattccggt gtatttttaa      300
tttaccaact ctgttataag aagaaaactt tcttaaattcc c                          341

```

<210> 286
 <211> 77
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> G682; polypeptide paralogous to G226

<400> 286

```

Met Asp Asn His Arg Arg Thr Lys Gln Pro Lys Thr Asn Ser Ile Val
1           5           10           15

```

```

Thr Ser Ser Ser Glu Gly Thr Glu Val Ser Ser Leu Glu Trp Glu Val
          20           25           30

```

```

Val Asn Met Ser Gln Glu Glu Glu Asp Leu Val Ser Arg Met His Lys
          35           40           45

```

```

Leu Val Gly Asp Arg Trp Glu Leu Ile Ala Gly Arg Ile Pro Gly Arg
          50           55           60

```

```

Thr Ala Gly Glu Ile Glu Arg Phe Trp Val Met Lys Asn
          65           70           75

```

<210> 287
 <211> 407
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <223> G226 Predicted polypeptide sequences is paralogous to G682

<400> 287

```

ccagtagtta tggataatac caaccgtctt cgtcttcgtc gcggtcccag tcttaggcaa      60
actaagttca ctcgatcccc atatgactct gaagaagtga gtagcatcga atgggagttt      120
atcagtatga ccgaacaaga agaagatctc atctctcgaa tgtacagact tgtcggtaat      180
agggtgggatt taatagcagg aagagtcgta ggaagaaagg caaatgagat tgagagatac      240
tggtattatga gaaactctga ctatttttct cacaaacgac gacgtcttaa taattctccc      300
tttttttcta cttctcctct taatctccaa gaaaatctaa aattgtaaag aatcaaaaat      360
aaaagctttc aatcataaaa gtagaacaaa tcttgaatgt cttctca                      407

```

<210> 288
 <211> 112
 <212> PRT

<213> Arabidopsis thaliana

<220>

<223> G226 polypeptide Paralogous to G682

<400> 288

Met Asp Asn Thr Asn Arg Leu Arg Leu Arg Arg Gly Pro Ser Leu Arg
1 5 10 15

Gln Thr Lys Phe Thr Arg Ser Arg Tyr Asp Ser Glu Glu Val Ser Ser
20 25 30

Ile Glu Trp Glu Phe Ile Ser Met Thr Glu Gln Glu Glu Asp Leu Ile
35 40 45

Ser Arg Met Tyr Arg Leu Val Gly Asn Arg Trp Asp Leu Ile Ala Gly
50 55 60

Arg Val Val Gly Arg Lys Ala Asn Glu Ile Glu Arg Tyr Trp Ile Met
65 70 75 80

Arg Asn Ser Asp Tyr Phe Ser His Lys Arg Arg Arg Leu Asn Asn Ser
85 90 95

Pro Phe Phe Ser Thr Ser Pro Leu Asn Leu Gln Glu Asn Leu Lys Leu
100 105 110

<210> 289

<211> 832

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G481 Predicted polypeptide sequence is paralogous to G482

<400> 289

gagcggtttcg tagaaaaatt cgatttctct aaagccctaa aactaaaacg actatcccca	60
attccaagtt ctagggtttc catcttcccc aatctagtat aaatggcgga tacgccttcg	120
agcccagctg gagatggcgg agaaagcggc ggttcogtta gggagcagga tcgatacctt	180
cctatagcta atatcagcag gatcatgaag aaagcggtgc ctcctaatgg taagattgga	240
aaagatgcta aggatacagt tcaggaatgc gtctctgagt tcatcagctt catcactagc	300
gaggccagtg ataagtgtca aaaagagaaa aggaaaactg tgaatggtga tgatttggtg	360
tgggcaatgg caacattagg atttgaggat tacctggaac ctctaaagat atacctagcg	420
aggtacaggg agttggaggg tgataataag ggatcaggaa agagtggaga tggatcaa	480
agagatgctg gtggcggtgt ttctggtgaa gaaatgccga gctggtaaaa gaagttgcaa	540
gtagtgatta agaacaatcg ccaa	600

tagttgagct gatcgacaac tatttcgggt ttactctcaa tttcgggttat gttagtttga 660
acgtttgggtt tattgtttcc gggttagttg gttgtattta aagatttctc tgtagatgt 720
tgagaacact tgaatgaagg aaaaatttgt ccacatcctg ttgttatttt cgattcactt 780
tcggaatttc atagctaatt tattctcatt taataccaaa tccttaaatt aa 832

<210> 290
<211> 141
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G481 polypeptide Paralogous to G482

<400> 290

Met Ala Asp Thr Pro Ser Ser Pro Ala Gly Asp Gly Gly Glu Ser Gly
1 5 10 15

Gly Ser Val Arg Glu Gln Asp Arg Tyr Leu Pro Ile Ala Asn Ile Ser
20 25 30

Arg Ile Met Lys Lys Ala Leu Pro Pro Asn Gly Lys Ile Gly Lys Asp
35 40 45

Ala Lys Asp Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile
50 55 60

Thr Ser Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Val
65 70 75 80

Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Asp
85 90 95

Tyr Leu Glu Pro Leu Lys Ile Tyr Leu Ala Arg Tyr Arg Glu Leu Glu
100 105 110

Gly Asp Asn Lys Gly Ser Gly Lys Ser Gly Asp Gly Ser Asn Arg Asp
115 120 125

Ala Gly Gly Gly Val Ser Gly Glu Glu Met Pro Ser Trp
130 135 140

<210> 291
<211> 1065
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G482 Predicted polypeptide sequence is paralogous to G481

<400> 291

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```

tcgacccacg cgtccggaca cttacaatt cacaccttct ctttttactc ttcctaaaac      60
cctaaatttc ctcgcttcag tcttccact caagtcaacc accaattgaa ttcgatttcg      120
aatcattgat ggaaatgatt tgaaaaaaga gtaaagttta tttttttatt ccttgtaatt      180
ttcagaaatg ggggattccg acagggattc cggaggaggg caaaacggga acaaccagaa      240
cggacagtcc tccttgtctc caagagagca agacaggttc ttgccgatcg ctaacgtcag      300
ccggatcatg aagaaggcct tgcccgccaa cgccaagatc tctaaagatg ccaaagagac      360
gatgcaggag tgtgtctccg agttcatcag cttcgtcacc ggagaagcat ctgataagtg      420
tcagaaggag aagaggaaga cgatcaacgg agacgatttg ctctgggcta tgactactct      480
aggttttgag gattatgttg agccattgaa agtttacttg cagaggttta gggagatcga      540
aggggagagg actggactag ggaggccaca gactggtggt gaggtcggag agcatcagag      600
agatgctgtc ggagatggcg gtgggttcta cgggtggtggt ggtgggatgc agtatcacca      660
acatcatcag tttcttcacc agcagaacca tatgtatgga gccacagggtg gcggtagcga      720
cagtggaggt ggagctgcct ccggtaggac aaggacttaa caaagattgg tgaagtggat      780
ctctctctgt atatagatac ataaatacat gtatacacat gcctattttt acgaccata      840
taaggatatc atcatgtgat agaacgaaca ttggtgttgg tgatgtaaaa tcagatgtgc      900
attaagggtt tagattttga ggctgtgtaa aagaagatca agtgtgcttt gttggacaat      960
aggattcact aacgaatctg cttcattgga tcttgtatgt aactaaagcc attgtattga     1020
atgcaaatgt tttcatttgg gatgctttaa aaaaaaaaaa aaaaaa                     1065

```

<210> 292

<211> 190

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G482 polypeptide Paralogous to G481

<400> 292

```

Met Gly Asp Ser Asp Arg Asp Ser Gly Gly Gly Gln Asn Gly Asn Asn
1           5           10           15

```

```

Gln Asn Gly Gln Ser Ser Leu Ser Pro Arg Glu Gln Asp Arg Phe Leu
          20           25           30

```

```

Pro Ile Ala Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn
          35           40           45

```

```

Ala Lys Ile Ser Lys Asp Ala Lys Glu Thr Met Gln Glu Cys Val Ser
          50           55           60

```

```

Glu Phe Ile Ser Phe Val Thr Gly Glu Ala Ser Asp Lys Cys Gln Lys

```

65

70

75

80

Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr
85 90 95

Thr Leu Gly Phe Glu Asp Tyr Val Glu Pro Leu Lys Val Tyr Leu Gln
100 105 110

Arg Phe Arg Glu Ile Glu Gly Glu Arg Thr Gly Leu Gly Arg Pro Gln
115 120 125

Thr Gly Gly Glu Val Gly Glu His Gln Arg Asp Ala Val Gly Asp Gly
130 135 140

Gly Gly Phe Tyr Gly Gly Gly Gly Gly Met Gln Tyr His Gln His His
145 150 155 160

Gln Phe Leu His Gln Gln Asn His Met Tyr Gly Ala Thr Gly Gly Gly
165 170 175

Ser Asp Ser Gly Gly Gly Ala Ala Ser Gly Arg Thr Arg Thr
180 185 190

<210> 293

<211> 684

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G485 Predicted polypeptide sequence is paralogous to G481 and G482

<400> 293

```
cctctctgat ccaacggacc caaaacatct atctctcttt ctcgaccttt tgtctcctcg      60
atctaaagat ggcggttcg gacaacgatt caggaggaca caaagacggt ggaaatgctt      120
cgacacgtga gcaagatagg tttctaccga tcgctaacgt tagcaggatc atgaagaaag      180
cacttcctgc gaacgcaaaa atctctaagg atgctaaaga aacggttcaa gagtgtgtat      240
cggaattcat aagtttcatc accggtgagg cttctgacaa gtgtcagaga gagaagagga      300
agacaatcaa cggtgacgat cttctttggg cgatgactac gctaggggtt gaggactacg      360
tggagcctct caaggtttat ctgcaaaagt atagggagggt ggaaggagag aagactacta      420
cggcaggggag acaaggcgat aaggaagggt gaggaggagg cggtggagct ggaagtggaa      480
gtggaggagc tccgatgtac ggtggtggca tggtgactac gatgggacat caattttccc      540
atcatttttc ttaattgtaa aatgataaaa gcaaattttc atttttatta attaatgata      600
tatatatata tatgtttaac ttttagtata atgtttacag aatttttttt ttaaaactag      660
gttcaaccca ctaacgtaac agcg                                684
```

<210> 294
 <211> 161
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> G485 polypeptide Paralogous to G481 and G482

<400> 294

Met Ala Asp Ser Asp Asn Asp Ser Gly Gly His Lys Asp Gly Gly Asn
 1 5 10 15

Ala Ser Thr Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Val Ser
 20 25 30

Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile Ser Lys Asp
 35 40 45

Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile
 50 55 60

Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile
 65 70 75 80

Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe Glu Asp
 85 90 95

Tyr Val Glu Pro Leu Lys Val Tyr Leu Gln Lys Tyr Arg Glu Val Glu
 100 105 110

Gly Glu Lys Thr Thr Thr Ala Gly Arg Gln Gly Asp Lys Glu Gly Gly
 115 120 125

Gly Gly Gly Gly Gly Ala Gly Ser Gly Ser Gly Gly Ala Pro Met Tyr
 130 135 140

Gly Gly Gly Met Val Thr Thr Met Gly His Gln Phe Ser His His Phe
 145 150 155 160

Ser

<210> 295
 <211> 476
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <223> G486 functionally related and homologous to G481 and G482

<400> 295

MBI0058CIP.ST25.txt

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 gccaatagcc aatgtaggga gacttatgaa gcaaataccta ccatcaaagc caaagatctc 120
 aaaagaagca aaacaaacag ttcaagaatg tgcaacagag ttcataagct ttgttacatg 180
 cgaagcatca gagaagtgcc acagggagaa tcggaagacg gtgaatggag acgacatctg 240
 gtgggctctc agcactctcg gcctcgataa ctatgctgac gccgtgggta ggcatcttca 300
 caagtaccgt gaagccgaga gagaaagaac tgagcacaac aaaggtagca atgatagtgg 360
 gaatgagaaa gaaaccaaca ctagaagtga tgtacagaac caatcgacaa aatttattag 420
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<210> 296

<211> 139

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G486 polypeptide functionally related and homologous to G481 and G482

<400> 296

Met Thr Asp Glu Asp Arg Leu Leu Pro Ile Ala Asn Val Gly Arg Leu
 1 5 10 15

Met Lys Gln Ile Leu Pro Ser Asn Ala Lys Ile Ser Lys Glu Ala Lys
 20 25 30

Gln Thr Val Gln Glu Cys Ala Thr Glu Phe Ile Ser Phe Val Thr Cys
 35 40 45

Glu Ala Ser Glu Lys Cys His Arg Glu Asn Arg Lys Thr Val Asn Gly
 50 55 60

Asp Asp Ile Trp Trp Ala Leu Ser Thr Leu Gly Leu Asp Asn Tyr Ala
 65 70 75 80

Asp Ala Val Gly Arg His Leu His Lys Tyr Arg Glu Ala Glu Arg Glu
 85 90 95

Arg Thr Glu His Asn Lys Gly Ser Asn Asp Ser Gly Asn Glu Lys Glu
 100 105 110

Thr Asn Thr Arg Ser Asp Val Gln Asn Gln Ser Thr Lys Phe Ile Arg
 115 120 125

Val Val Glu Lys Gly Ser Ser Ser Ser Ala Arg
 130 135

<210> 297
 <211> 1473
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <223> G1067 Predicted polypeptide sequence is paralogous to G1073

```

<400> 297
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tcttaccttt catgagagag atcatttaac ataagtcacc ttttttatat cttttgcttc      180
gtctttaatt tagttctggt cttgggtctgt ttctatatatt tgtcggcttg cgtaaccgat      240
cacaccttaa tgcttttagct attgtttcct caaaatcatg agttttgact tctcgatctg      300
agttttcttt ttctctcttt acgctcttct tcacctagct accaatatat gaacgagcag      360
gatcaagaat cgagaaattg atttgagctg gcgaataagc agtgggtggga tagggaatta      420
gtagatgcgg cggcgatgga aggcggttac gagcaaggcg gtggagcttc tagatacttc      480
cataacctct ttagaccgga gattcaccac caacagcttc aaccgcaggg cgggatcaat      540
cttatcgacc agcatcatca tcagcaccag caacatcaac aacaacaaca accgtcggat      600
gattcaagag aatctgacca ttcaaacaaa gatcatcatc aacagggtcg acccgattca      660
gacccgaata catcaagctc agcaccggga aaacgtccac gtggacgtcc accaggatct      720
aagaacaaag ccaagccacc gatcatagta actcgtgata gcccacacgc gcttagatct      780
cacgttcttg aagtatctcc tggagctgac atagttgaga gtgtttccac gtacgctagg      840
aggagagggg gaggcgtctc cgtttttagg ggaacaggca cgtatctaa cgtcactctc      900
cgtcagccag tctctcctgg aaatggcggg ggtgtgtccg gagggaggagg agttgtgact      960
ttacatggaa ggtttgagat tctttcgcta acggggactg ttttgccacc tcctgcaccg     1020
cctggtgccg gtggtttgtc tatattttta gccggagggc aagggtcagg ggtcggagga     1080
agcgttgtgg ctccccttat tgcatcagct ccggttatac taatggcggc ttcgttctca     1140
aatgcggttt tcgagagact accgattgag gaggaggaag aagaaggtgg tgggtggcgg     1200
ggaggaggag gaggagggcc accgcagatg caacaagctc catcagcatc tccgccgtct     1260
ggagtgaccg gtcagggaca gttaggaggt aatgtgggtg gttatgggtt ttctggtgat     1320
cctcatattg ttggatgggg agctggaaca ccttcaagac caccttttta attgaatttt     1380
aatgtccgga aatttatgtg tttttatcat cttgaggagt cgtctttcct ttgggatatt     1440
tggtgtttta tgtttagttg atatgcatat ttt                                     1473
    
```

<210> 298
 <211> 311
 <212> PRT
 <213> Arabidopsis thaliana

<220>

<223> G1067 polypeptide Paralogous to G1073

<400> 298

Met Glu Gly Gly Tyr Glu Gln Gly Gly Gly Ala Ser Arg Tyr Phe His
 1 5 10 15

Asn Leu Phe Arg Pro Glu Ile His His Gln Gln Leu Gln Pro Gln Gly
 20 25 30

Gly Ile Asn Leu Ile Asp Gln His His His Gln His Gln Gln His Gln
 35 40 45

Gln Gln Gln Gln Pro Ser Asp Asp Ser Arg Glu Ser Asp His Ser Asn
 50 55 60

Lys Asp His His Gln Gln Gly Arg Pro Asp Ser Asp Pro Asn Thr Ser
 65 70 75 80

Ser Ser Ala Pro Gly Lys Arg Pro Arg Gly Arg Pro Pro Gly Ser Lys
 85 90 95

Asn Lys Ala Lys Pro Pro Ile Ile Val Thr Arg Asp Ser Pro Asn Ala
 100 105 110

Leu Arg Ser His Val Leu Glu Val Ser Pro Gly Ala Asp Ile Val Glu
 115 120 125

Ser Val Ser Thr Tyr Ala Arg Arg Arg Gly Arg Gly Val Ser Val Leu
 130 135 140

Gly Gly Asn Gly Thr Val Ser Asn Val Thr Leu Arg Gln Pro Val Thr
 145 150 155 160

Pro Gly Asn Gly Gly Gly Val Ser Gly Gly Gly Gly Val Val Thr Leu
 165 170 175

His Gly Arg Phe Glu Ile Leu Ser Leu Thr Gly Thr Val Leu Pro Pro
 180 185 190

Pro Ala Pro Pro Gly Ala Gly Gly Leu Ser Ile Phe Leu Ala Gly Gly
 195 200 205

Gln Gly Gln Val Val Gly Gly Ser Val Val Ala Pro Leu Ile Ala Ser
 210 215 220

Ala Pro Val Ile Leu Met Ala Ala Ser Phe Ser Asn Ala Val Phe Glu
 225 230 235 240

MBI0058CIP.ST25.txt

Arg Leu Pro Ile Glu Glu Glu Glu Glu Glu Gly Gly Gly Gly Gly Gly
245 250 255

Gly Gly Gly Gly Gly Pro Pro Gln Met Gln Gln Ala Pro Ser Ala Ser
260 265 270

Pro Pro Ser Gly Val Thr Gly Gln Gly Gln Leu Gly Gly Asn Val Gly
275 280 285

Gly Tyr Gly Phe Ser Gly Asp Pro His Leu Leu Gly Trp Gly Ala Gly
290 295 300

Thr Pro Ser Arg Pro Pro Phe
305 310

<210> 299
<211> 1295
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G1070 Functionally related and homologous to G1073

<400> 299
tcgaccagct tggatttcgt tgttcacat tactactctc tttcttcttc tagctagcta 60
gttttgacag caaaataaga agcaaaaaa aggtcaacta aaaaagatct gttcttagat 120
cactctcttc ttcttttttt gatccaattc caccattgaa tcatagatca tggatccagt 180
acaatctcat ggatcacaaa gctctctacc tctctcttc cacgcaagag actttcaatt 240
acatcttcaa caacagcaac aagagttctt cctccaccat caccagcaac aaagaaacca 300
aaccgatggg gaccaacaag gaggatcagg aggaaaccga caaatcaaga tggatcgtga 360
agagacaagc gacaacatag acaacatagc taacaacagc ggtagtgaag gtaaagacat 420
agatatacac ggtgggttcag gagaaggagg tgggtggctcc ggaggagatc atcagatgac 480
aagaagacca agaggaagac cagcgggatc caagaacaaa ccaaaaccac cgattatcat 540
cacacgggac agcgcaaagc cgcttagaac ccacgtgatg gagatcggag atggctgcga 600
cttagtcgaa agcgttgcc a ttttgcacg aagacgcaa cgcgcggtt gcgttatgag 660
cggtactgga aatgttacta acgtcactat acgtcagcct ggatctcatc cttctctg 720
ctcggtagtt agtcttcacg gaagggtcga gattctatct ctctcaggat cttttctccc 780
tctccgggt cctcctacag ccaccggatt gagtgtttac ctgctggag gacaaggaca 840
gggtggttga ggaagcgtag ttggtccgtt gttatgtgct ggtcctgtcg ttgtcatggc 900
tgcgctcttt agcaatgcgg cgtacgaaag gttgccttta gaggaagatg agatgcagac 960
gccggttcat ggcggaggag gaggaggatc attggagtcg ccgccaatga tgggacaaca 1020

actgcaacat cagcaacaag ctatgtcagg tcatcaaggg ttaccaccta atcttcttgg 1080
 ttcggttcag ttgcagcagc aacatgatca gtcttattgg tcaacggggac gaccaccgta 1140
 ttgatcaaata atacacacac actcataatc gttgctagct agctaacgat gaatcatgag 1200
 tttagtggat atatatatga ttaaaagagg ttagcttatg aacattaata agagtttgga 1260
 ttctatcgag cttcattatg tttgggtcat cgttc 1295

<210> 300

<211> 324

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G1070 polypeptide Functionally related and homologous to G1073

<400> 300

Met Asp Pro Val Gln Ser His Gly Ser Gln Ser Ser Leu Pro Pro Pro
 1 5 10 15

Phe His Ala Arg Asp Phe Gln Leu His Leu Gln Gln Gln Gln Gln Glu
 20 25 30

Phe Phe Leu His His His Gln Gln Gln Arg Asn Gln Thr Asp Gly Asp
 35 40 45

Gln Gln Gly Gly Ser Gly Gly Asn Arg Gln Ile Lys Met Asp Arg Glu
 50 55 60

Glu Thr Ser Asp Asn Ile Asp Asn Ile Ala Asn Asn Ser Gly Ser Glu
 65 70 75 80

Gly Lys Asp Ile Asp Ile His Gly Gly Ser Gly Glu Gly Gly Gly Gly
 85 90 95

Ser Gly Gly Asp His Gln Met Thr Arg Arg Pro Arg Gly Arg Pro Ala
 100 105 110

Gly Ser Lys Asn Lys Pro Lys Pro Pro Ile Ile Ile Thr Arg Asp Ser
 115 120 125

Ala Asn Ala Leu Arg Thr His Val Met Glu Ile Gly Asp Gly Cys Asp
 130 135 140

Leu Val Glu Ser Val Ala Thr Phe Ala Arg Arg Arg Gln Arg Gly Val
 145 150 155 160

Cys Val Met Ser Gly Thr Gly Asn Val Thr Asn Val Thr Ile Arg Gln
 165 170 175

MBI0058CIP.ST25.txt

Pro Gly Ser His Pro Ser Pro Gly Ser Val Val Ser Leu His Gly Arg
180 185 190

Phe Glu Ile Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala Pro
195 200 205

Pro Thr Ala Thr Gly Leu Ser Val Tyr Leu Ala Gly Gly Gln Gly Gln
210 215 220

Val Val Gly Gly Ser Val Val Gly Pro Leu Leu Cys Ala Gly Pro Val
225 230 235 240

Val Val Met Ala Ala Ser Phe Ser Asn Ala Ala Tyr Glu Arg Leu Pro
245 250 255

Leu Glu Glu Asp Glu Met Gln Thr Pro Val His Gly Gly Gly Gly Gly
260 265 270

Gly Ser Leu Glu Ser Pro Pro Met Met Gly Gln Gln Leu Gln His Gln
275 280 285

Gln Gln Ala Met Ser Gly His Gln Gly Leu Pro Pro Asn Leu Leu Gly
290 295 300

Ser Val Gln Leu Gln Gln Gln His Asp Gln Ser Tyr Trp Ser Thr Gly
305 310 315 320

Arg Pro Pro Tyr

<210> 301

<211> 974

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G1073 reference sequence

<400> 301

ccccccgacc tgcctctaca gagacctgaa gattccagaa cccacactga tcaaaaataa 60

catggaactt aacagatctg aagcagacga agcaaaggcc gagaccactc ccaccggttg 120

agccaccagc tcagccacag cctctggctc ttcctccgga cgctcgccac gtggctcgcc 180

tgcaggttcc aaaaacaaac ccaaactcc gacgattata actagagata gtcctaactg 240

ccttagatca cacgttcttg aagtcacctc cggttcggac atatccgagg cagtctccac 300

ctacgccact cgctcgggct gcggcgtttg cattataagc ggcacgggtg cggtcactaa 360

cgtcacgata cggcaacctg cggctccggc tgggtggagg gtgattacc tgcattggtc 420

MBI0058CIP.ST25.txt

```

gtttgacatt ttgtctttga ccggtactgc gcttccaccg cctgcaccac cgggagcagg 480
aggtttgacg gtgtatctag ccggagggtca aggacaagtt gtaggaggga atgtggctgg 540
ttcgттаatt gcttcgggac cggtagtgtt gatggctgct tcttttgcaa acgcagttta 600
tgataggtta ccgattgaag aggaagaaac cccaccgccg agaaccaccg ggggtgcagca 660
gcagcagccg gaggcgtctc agtcgtcgga ggttacgggg agtggggccc aggcgtgtga 720
gtcaaacctc caaggtggaa atggtggagg aggtgttgct ttctacaatc ttggaatgaa 780
tatgaacaat tttcaattct ccggggggaga tatttacggg atgagcggcg gtagcggagg 840
agggtgggtggc ggtgcgacta gacccgcggt ttagagtttt agcgttttgg tgacaccttt 900
tgttgcgttt gcgtgtttga cctcaaacta ctaggctact agctatagcg gttgcgaaat 960
gcgaatatta ggtt 974

```

<210> 302

<211> 270

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G1073 polypeptide reference sequence

<400> 302

```

Met Glu Leu Asn Arg Ser Glu Ala Asp Glu Ala Lys Ala Glu Thr Thr
1           5           10           15

```

```

Pro Thr Gly Gly Ala Thr Ser Ser Ala Thr Ala Ser Gly Ser Ser Ser
          20           25           30

```

```

Gly Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys Asn Lys Pro Lys
          35           40           45

```

```

Pro Pro Thr Ile Ile Thr Arg Asp Ser Pro Asn Val Leu Arg Ser His
50           55           60

```

```

Val Leu Glu Val Thr Ser Gly Ser Asp Ile Ser Glu Ala Val Ser Thr
65           70           75           80

```

```

Tyr Ala Thr Arg Arg Gly Cys Gly Val Cys Ile Ile Ser Gly Thr Gly
          85           90           95

```

```

Ala Val Thr Asn Val Thr Ile Arg Gln Pro Ala Ala Pro Ala Gly Gly
          100          105          110

```

```

Gly Val Ile Thr Leu His Gly Arg Phe Asp Ile Leu Ser Leu Thr Gly
115           120           125

```

MBI0058CIP.ST25.txt

Thr Ala Leu Pro Pro Pro Ala Pro Pro Gly Ala Gly Gly Leu Thr Val
130 135 140

Tyr Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly Asn Val Ala Gly
145 150 155 160

Ser Leu Ile Ala Ser Gly Pro Val Val Leu Met Ala Ala Ser Phe Ala
165 170 175

Asn Ala Val Tyr Asp Arg Leu Pro Ile Glu Glu Glu Glu Thr Pro Pro
180 185 190

Pro Arg Thr Thr Gly Val Gln Gln Gln Gln Pro Glu Ala Ser Gln Ser
195 200 205

Ser Glu Val Thr Gly Ser Gly Ala Gln Ala Cys Glu Ser Asn Leu Gln
210 215 220

Gly Gly Asn Gly Gly Gly Gly Val Ala Phe Tyr Asn Leu Gly Met Asn
225 230 235 240

Met Asn Asn Phe Gln Phe Ser Gly Gly Asp Ile Tyr Gly Met Ser Gly
245 250 255

Gly Ser Gly Gly Gly Gly Gly Gly Ala Thr Arg Pro Ala Phe
260 265 270

<210> 303
<211> 1084
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G1075 Functionally related and homologous to G1073

<400> 303
tttgtgtttg gtgctggcat ggctggtctc gatctaggca caacttctcg ctacgtccac 60
aacgtcgatg gtggcggcgg cggacagttc accaccgaca accaccacga agatgacggt 120
ggcgctggag gaaaccacca tcatcaccat cataatcata atcaccatca aggttttagat 180
ttaatagctt ctaatgataa ctctggacta ggcggcgggtg gaggaggagg gagcggtgac 240
ctcgtcatgc gtcggccacg tggccgtcca gctggatcga agaacaaacc gaagccgccg 300
gtgattgtca cgcgcgagag cgcaaact cttagggctc acattcttga agttggaagt 360
ggctgcgacg ttttcgaatg tatctccact tacgctcgtc ggagacagcg cgggatttgc 420
gttttatccg ggacgggaac cgtcactaac gtcagcatcc gtcagcctac ggcggccgga 480
gctgtttgtga ctctgcgggg tacttttgag attctttccc tctccggatc ttttcttccg 540
ccacctgctc ctccaggggc gactagcttg acgatattcc tcgctggagc tcaaggacag 600

MBI0058CIP.ST25.txt

```

gtcgtcggag gtaacgtagt tggtagagta atggcgccgg gcccggtaat ggtcatggca    660
gcgtcttttta caaacgtggc ttacgaaagg ttgcctttgg acgagcatga ggagcacttg    720
caaagtggcg gcggcggagg tggaggggaat atgtactcgg aagccactgg cgggtggcga    780
gggttgccctt tctttaattt gccgatgagt atgcctcaga ttggagttga aagttggcag    840
gggaatcacg ccggcgccgg tagggctccg ttttagcaat ttaagaaaact ttaattgttt    900
tttccactttt tttgtttttc tccgaatttt atgaaattat gatttaagaa aaaaaacgat    960
attgttcacg tattgacctt cttactgcat gggtttcttct attgggttaa ttggctagct   1020
cataagaatt gttaatttg gttattgtca tcaaatttgc ccacatataa agcttctagc   1080
aaat                                                                    1084

```

<210> 304

<211> 285

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G1075 polypeptide Functionally related and homologous to G1073

<400> 304

```

Met Ala Gly Leu Asp Leu Gly Thr Thr Ser Arg Tyr Val His Asn Val
1           5           10           15

```

```

Asp Gly Gly Gly Gly Gly Gln Phe Thr Thr Asp Asn His His Glu Asp
          20           25           30

```

```

Asp Gly Gly Ala Gly Gly Asn His His His His His Asn His Asn
          35           40           45

```

```

His His Gln Gly Leu Asp Leu Ile Ala Ser Asn Asp Asn Ser Gly Leu
          50           55           60

```

```

Gly Gly Gly Gly Gly Gly Gly Ser Gly Asp Leu Val Met Arg Arg Pro
65           70           75           80

```

```

Arg Gly Arg Pro Ala Gly Ser Lys Asn Lys Pro Lys Pro Pro Val Ile
          85           90           95

```

```

Val Thr Arg Glu Ser Ala Asn Thr Leu Arg Ala His Ile Leu Glu Val
          100          105          110

```

```

Gly Ser Gly Cys Asp Val Phe Glu Cys Ile Ser Thr Tyr Ala Arg Arg
          115          120          125

```

```

Arg Gln Arg Gly Ile Cys Val Leu Ser Gly Thr Gly Thr Val Thr Asn
          130          135          140

```

Val Ser Ile Arg Gln Pro Thr Ala Ala Gly Ala Val Val Thr Leu Arg
145 150 155 160

Gly Thr Phe Glu Ile Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro Pro
165 170 175

Ala Pro Pro Gly Ala Thr Ser Leu Thr Ile Phe Leu Ala Gly Ala Gln
180 185 190

Gly Gln Val Val Gly Gly Asn Val Val Gly Glu Leu Met Ala Ala Gly
195 200 205

Pro Val Met Val Met Ala Ala Ser Phe Thr Asn Val Ala Tyr Glu Arg
210 215 220

Leu Pro Leu Asp Glu His Glu Glu His Leu Gln Ser Gly Gly Gly Gly
225 230 235 240

Gly Gly Gly Asn Met Tyr Ser Glu Ala Thr Gly Gly Gly Gly Gly Leu
245 250 255

Pro Phe Phe Asn Leu Pro Met Ser Met Pro Gln Ile Gly Val Glu Ser
260 265 270

Trp Gln Gly Asn His Ala Gly Ala Gly Arg Ala Pro Phe
275 280 285

<210> 305
<211> 1342
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G1076 Functionally related and homologous to G1073

<400> 305
atatttagtct tcctataact tcttctcaat cctctctcat atcttttttc ttagtttaaa 60
tttcaataaa atagaaaaaa acatatacaa atctacagag aagagaagct ttattttaat 120
cttgtgtgtg tgtgtgtgtt ttatataatt tttatttttt ttcaaattaa aatctcttct 180
ttgcttttga tgtgggcatg gctggctctg atctaggcac agcttttcgt tacgttaatc 240
accagctcca tcgtcccgat ctccaccttc accacaattc ctccctccgat gacgtcactc 300
ccggagccgg gatgggtcat ttcaccgtcg acgacgaaga caacaacaac aaccatcaag 360
gtcttgactt agcctctggt ggaggatcag gaagctctgg aggaggagga ggtcacggcg 420
ggggaggaga cgtcgttggt cgtcgtccac gtggcagacc accgggatcc aagaacaaac 480
cgaaacctcc ggtaattatc acgcgcgaga gcgcaaacac tctaagagct cacattcttg 540

MBI0058CIP.ST25.txt

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aagtaacaaa cggctgcat gttttcgact gcgttgogac ttatgctcgt cggagacagc 600
gagggatctg cgttctgagc ggtagcggaa cggtcacgaa cgtcagcata cgtcagccat 660
ctgcggctgg agcgggttg acgctacaag gaacgttcga gattctttct ctctccggat 720
cgtttcttcc tcttccggca cctcccggag caacgagttt gacaattttc ttagccggag 780
gacaaggtca ggtggttgga ggaagcggtg tgggtgagct tacggcggct ggaccgggtga 840
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agcagcagca acagcttgga ggaggatcta acggcggagg taatttggtt cgggaggtgg 960
cagctggagg aggaggagga cttccgttct ttaatttacc gatgaatatg caaccaaagt 1020
tgcaacttcc ggtggaaggt tggccgggga attccggtgg aagaggtcct ttctgatgtg 1080
tatatatga taatcattat atatataccg gcggagaagc ttttccggcg aagaatttgc 1140
gagagtgaag aaagggttaga aaagctttta atggactaat gaatttcaaa ttatcatcgt 1200
gatttcggac attgtcttgt tcatcatgtt aagcttaggt ttattttttg tcgtttgtag 1260
aattttatgt ttgaatcctt ttttttttct gtgaaactct attgtgttcg tctgcgaagg 1320
aaaaaaaaat tctcaaaaaa aa 1342

```

<210> 306

<211> 292

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G1076 polypeptide Functionally related and homologous to G1073

<400> 306

```

Met Ala Gly Leu Asp Leu Gly Thr Ala Phe Arg Tyr Val Asn His Gln
1          5          10          15

```

```

Leu His Arg Pro Asp Leu His Leu His His Asn Ser Ser Ser Asp Asp
          20          25          30

```

```

Val Thr Pro Gly Ala Gly Met Gly His Phe Thr Val Asp Asp Glu Asp
          35          40          45

```

```

Asn Asn Asn Asn His Gln Gly Leu Asp Leu Ala Ser Gly Gly Gly Ser
50          55          60

```

```

Gly Ser Ser Gly Gly Gly Gly Gly His Gly Gly Gly Gly Asp Val Val
65          70          75          80

```

```

Gly Arg Arg Pro Arg Gly Arg Pro Pro Gly Ser Lys Asn Lys Pro Lys
          85          90          95

```

MBI0058CIP.ST25.txt

Pro Pro Val Ile Ile Thr Arg Glu Ser Ala Asn Thr Leu Arg Ala His
100 105 110

Ile Leu Glu Val Thr Asn Gly Cys Asp Val Phe Asp Cys Val Ala Thr
115 120 125

Tyr Ala Arg Arg Arg Gln Arg Gly Ile Cys Val Leu Ser Gly Ser Gly
130 135 140

Thr Val Thr Asn Val Ser Ile Arg Gln Pro Ser Ala Ala Gly Ala Val
145 150 155 160

Val Thr Leu Gln Gly Thr Phe Glu Ile Leu Ser Leu Ser Gly Ser Phe
165 170 175

Leu Pro Pro Pro Ala Pro Pro Gly Ala Thr Ser Leu Thr Ile Phe Leu
180 185 190

Ala Gly Gly Gln Gly Gln Val Val Gly Gly Ser Val Val Gly Glu Leu
195 200 205

Thr Ala Ala Gly Pro Val Ile Val Ile Ala Ala Ser Phe Thr Asn Val
210 215 220

Ala Tyr Glu Arg Leu Pro Leu Glu Glu Asp Glu Gln Gln Gln Gln Leu
225 230 235 240

Gly Gly Gly Ser Asn Gly Gly Gly Asn Leu Phe Pro Glu Val Ala Ala
245 250 255

Gly Gly Gly Gly Gly Leu Pro Phe Phe Asn Leu Pro Met Asn Met Gln
260 265 270

Pro Asn Val Gln Leu Pro Val Glu Gly Trp Pro Gly Asn Ser Gly Gly
275 280 285

Arg Gly Pro Phe
290

<210> 307

<211> 483

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G1248 Functionally related and homologous to G481 and G482

<400> 307

atggcgggga attatcattc gttccaaaat ccaatccctc gataccagaa ttacaacttc 60

gggagcagct catctaata tcaacatgaa catgatgggt tagtggtggt ggtggaggat 120

MBI0058CIP.ST25.txt

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caacagcaag aagaaagcat gatggtaaaa gaacaagaca ggctacttcc gatagcaaac 180
gtaggaagga tcatgaagaa catcctccca gcaaacgcaa aggtctctaa agaagccaaa 240
gagactatgc aagaatgtgt gtccgagttc attagcttcg tcacgggaga agcatccgat 300
aaatgccaca aggagaagcg aaagaccggt aatggagacg atatctgttg ggctatggct 360
aatctagggg ttgatgatta cgccgcccag ctcaagaagt acttacatcg ttaccgagtt 420
ctcgaagggt agaaacctaa tcatcacggc aaaggaggac ctaaatactc gccagataat 480
taa 483

```

<210> 308

<211> 160

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G1248 polypeptide Functionally related and homologous to G481 and G482

<400> 308

```

Met Ala Gly Asn Tyr His Ser Phe Gln Asn Pro Ile Pro Arg Tyr Gln
1           5           10           15

```

```

Asn Tyr Asn Phe Gly Ser Ser Ser Ser Asn His Gln His Glu His Asp
          20           25           30

```

```

Gly Leu Val Val Val Val Glu Asp Gln Gln Gln Glu Glu Ser Met Met
          35           40           45

```

```

Val Lys Glu Gln Asp Arg Leu Leu Pro Ile Ala Asn Val Gly Arg Ile
          50           55           60

```

```

Met Lys Asn Ile Leu Pro Ala Asn Ala Lys Val Ser Lys Glu Ala Lys
65           70           75           80

```

```

Glu Thr Met Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr Gly
          85           90           95

```

```

Glu Ala Ser Asp Lys Cys His Lys Glu Lys Arg Lys Thr Val Asn Gly
          100          105          110

```

```

Asp Asp Ile Cys Trp Ala Met Ala Asn Leu Gly Phe Asp Asp Tyr Ala
          115          120          125

```

```

Ala Gln Leu Lys Lys Tyr Leu His Arg Tyr Arg Val Leu Glu Gly Glu
          130          135          140

```

```

Lys Pro Asn His His Gly Lys Gly Gly Pro Lys Ser Ser Pro Asp Asn

```

145

150

155

160

<210> 309
<211> 823
<212> DNA
<213> Arabidopsis thaliana

<220>

<223> G1364 Predicted polypeptide sequence is paralogous to G481 and G482

<400> 309
ctctttctctc gatctctctc cctctctgcc tcctctcttc ctccaatcaa caaacacctc 60
tctgtttcac tcccgccctt tttcgaattc ttctgatggc ggagtcgcag gccaagagtc 120
ccggaggctg tggaagccat gagagtgggtg gagatcaaag tcccaggctc ttacatgttc 180
gtgagcaaga taggtttctt ccgattgcta acataagccg tatcatgaaa agaggtcttc 240
ctgctaattg gaaaatcgct aaagatgcta aggagattgt gcaggaatgt gtctctgaat 300
tcatcagttt cgtcaccagc gaagcgagtg ataaatgtca aagagagaaa aggaagacta 360
ttaatggaga tgatttgctt tgggcaatgg ctactttagg atttgaagac tacatggaac 420
ctctcaaggt ttacctgatg agatatagag agatggaggg tgacacaaag ggatcagcaa 480
aaggtgggga tccaaatgca aagaaagatg ggcaatcaag ccaaaatggc cagttctcgc 540
agcttgctca ccaaggtcct tatgggaact ctcaagctca gcagcatatg atggttccaa 600
tgccgggaac agactagtat gagaggagta ttcaactttg gttatgttcc accaaaagag 660
gttatcttat ctgtatatta tttgtgttgt aagagttttg ctatgcagaa cttgtgacta 720
taatcatctc attgttttgt tttgtttttg tttccttgga tttgttctga atatgtcatc 780
aagtcagtca gtctatttat atatttggtt tgttgattat ttc 823

<210> 310
<211> 173
<212> PRT
<213> Arabidopsis thaliana

<220>

<223> G1364 polypeptide Paralogous to G481 and G482

<400> 310

Met Ala Glu Ser Gln Ala Lys Ser Pro Gly Gly Cys Gly Ser His Glu
1 5 10 15

Ser Gly Gly Asp Gln Ser Pro Arg Ser Leu His Val Arg Glu Gln Asp
20 25 30

Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Arg Gly Leu
35 40 45

Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu Ile Val Gln Glu

50		55		60
Cys Val Ser Glu Phe Ile Ser Phe Val Thr Ser Glu Ala Ser Asp Lys				
65		70		75 80
Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp				
	85		90	95
Ala Met Ala Thr Leu Gly Phe Glu Asp Tyr Met Glu Pro Leu Lys Val				
	100		105	110
Tyr Leu Met Arg Tyr Arg Glu Met Glu Gly Asp Thr Lys Gly Ser Ala				
	115		120	125
Lys Gly Gly Asp Pro Asn Ala Lys Lys Asp Gly Gln Ser Ser Gln Asn				
	130		135	140
Gly Gln Phe Ser Gln Leu Ala His Gln Gly Pro Tyr Gly Asn Ser Gln				
145		150		155 160
Ala Gln Gln His Met Met Val Pro Met Pro Gly Thr Asp				
	165		170	

<210> 311
 <211> 757
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <223> G1781 Functionally related and homologous to G481 and G482

<400> 311	
cgctcgaccag attgatcaca tgttggttaac atcaatcaaa aaaaaaaca aagagataga	60
gatatgactg aggagagccc agaagaagat catgggtctc ctggagtagc tgaacaaat	120
ccaggaagcc cttcttcaaa gaccaacaac aacaacaaca acaacaaga acaagaccgg	180
tttcttccca ttgcgaatgt cggaaggatc atgaaaaaag ttcttcccgg taacggtaag	240
atctcaaaag acgctaaaga aaccgttcaa gaatgtgtct cggagttcat tagtttcgtc	300
actggtgaag cttctgacaa gtgtcaaaga gaaaagagga agaccatcaa tggagatgat	360
atcatttggg ctatcacaac tctcggtttc gaagactacg tggctccatt aaaggtctac	420
ctctgcaaat atagagacac cgaaggagag aaagttaaca gcccaaaaca acaacaaca	480
agacaacaac aacagcagat tcaacaacag aatcatcata attatcagtt tcaagaaca	540
gacaaaaca ataacaacat gtcattgtact agttacatct ctcatcatca tccttctcca	600
ttcctaaccag tggatcatca accttttccc aatattgctt tctctcctaa atcattgcag	660
aaacagttcc cgcagcagca tgataataac attgattcaa ttcactggtg agagagacat	720

ttgcttgccg gccgctctag gcgggaaaag cccgaat

757

<210> 312

<211> 215

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G1781 polypeptide Functionally related and homologous to G481 and G482

<400> 312

Met Thr Glu Glu Ser Pro Glu Glu Asp His Gly Ser Pro Gly Val Ala
1 5 10 15

Glu Thr Asn Pro Gly Ser Pro Ser Ser Lys Thr Asn Asn Asn Asn Asn
20 25 30

Asn Asn Lys Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Val Gly Arg
35 40 45

Ile Met Lys Lys Val Leu Pro Gly Asn Gly Lys Ile Ser Lys Asp Ala
50 55 60

Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr
65 70 75 80

Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn
85 90 95

Gly Asp Asp Ile Ile Trp Ala Ile Thr Thr Leu Gly Phe Glu Asp Tyr
100 105 110

Val Ala Pro Leu Lys Val Tyr Leu Cys Lys Tyr Arg Asp Thr Glu Gly
115 120 125

Glu Lys Val Asn Ser Pro Lys Gln Gln Gln Gln Arg Gln Gln Gln Gln
130 135 140

Gln Ile Gln Gln Gln Asn His His Asn Tyr Gln Phe Gln Glu Gln Asp
145 150 155 160

Gln Asn Asn Asn Asn Met Ser Cys Thr Ser Tyr Ile Ser His His His
165 170 175

Pro Ser Pro Phe Leu Pro Val Asp His Gln Pro Phe Pro Asn Ile Ala
180 185 190

Phe Ser Pro Lys Ser Leu Gln Lys Gln Phe Pro Gln Gln His Asp Asn
195 200 205

Asn Ile Asp Ser Ile His Trp
210 215

<210> 313
<211> 318
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G1816 Predicted polypeptide sequence is paralogous to G682 and G226

<400> 313
atggataaca ctgaccgtcg tcgccgtcgt aagcaacaca aaatcgccct ccatgactct 60
gaagtgagca gtatcgaatg ggagtttatc aacatgactg aacaagaaga agatctcatc 120
tttcgaatgt acagacttgt cggatgatagg tgggatttga tagcaggaag agttcctgga 180
agacaaccag aggagataga gagatattgg ataatgagaa acagtgaagg ctttgctgat 240
aaacgacgcc agcttcactc atcttccac aaacatacca agcctcaccg tcctcgcttt 300
tctatctatc cttcctag 318

<210> 314
<211> 105
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G1816 polypeptide Paralogous to G682 and G226

<400> 314

Met Asp Asn Thr Asp Arg Arg Arg Arg Arg Lys Gln His Lys Ile Ala
1 5 10 15

Leu His Asp Ser Glu Val Ser Ser Ile Glu Trp Glu Phe Ile Asn Met
20 25 30

Thr Glu Gln Glu Glu Asp Leu Ile Phe Arg Met Tyr Arg Leu Val Gly
35 40 45

Asp Arg Trp Asp Leu Ile Ala Gly Arg Val Pro Gly Arg Gln Pro Glu
50 55 60

Glu Ile Glu Arg Tyr Trp Ile Met Arg Asn Ser Glu Gly Phe Ala Asp
65 70 75 80

Lys Arg Arg Gln Leu His Ser Ser Ser His Lys His Thr Lys Pro His
85 90 95

Arg Pro Arg Phe Ser Ile Tyr Pro Ser
100 105

<210> 315
 <211> 1130
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <223> G1945 Functionally related and homologous to G1073

<400> 315
 atttcccaaa gggatttacg aaaagtcctt ctctctatc atctctttat tcaccccata 60
 ccaacaacct ctacatcttc ttcttcttct tctctctctt ttattttctt tttaaatacat 120
 ttacacaaaa atccaaagac aaatctgaaa tctctaataa acaaataccat aaaataagaa 180
 aaacaaagat gaaagggtgaa tacagagagc aaaagagtaa cgaaatgttt tccaagcttc 240
 ctcatcatca acaacaacag caacaacaac aacaacaaca ctctcttacc tctcacttcc 300
 acctctctc caccgtaacc cccaccgtcg atgactctc catcgaagtg gtccgacgtc 360
 cacgtggcag accaccaggt tccaaaaaca aacctaaacc acccgtcttc gtcacacgtg 420
 acaccgacct tcctatgagt ccttacatcc tcgaagtctc ttcaggaaac gacgtcgtcg 480
 aagccatcaa ccgtttctgc cgccgtaa atcatcgaggt ctgcgtcctt agtggctctg 540
 gctctgtagc taacgtcact ttacgtcagc catcaccggc agctcttggc tctaccataa 600
 ctttccatgg aaagtgtgat ctctctcctg tctccgcaac gtttctcctt cctccgcctc 660
 gtacttcctt gtctcctccc gtttctaact tcttcaccgt ctctctcgct ggacctcaag 720
 gacaaatcat cggagggttc gtcgctggtc cacttatctt gccaggaaca gtttacgtca 780
 tcgccycaag tttcaacaac ccttcttctc accggttacc gccggaagaa gagcaaaaac 840
 actcggcggg gacaggggaa agagagggac aatctccgcc ggtctctggt gccggtgaag 900
 agtcaggaca gatggcgagg agtggaggag agtcgtgtgg ggtatcaatg tacagttgcc 960
 acatgggtgg ctctgatgtt atttgggccc ctacagccag agctccaccg ccataactaac 1020
 caatccttct ttcacaaatc tctttcttct tttttttggt tttttttggt ttggggttagg 1080
 atgaatcaag aaactagggt tttttttttt ttttttttaa aaaaaaaaaa 1130

<210> 316
 <211> 276
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> G1945 polypeptide Functionally related and homologous to G1073

<400> 316

Met Lys Gly Glu Tyr Arg Glu Gln Lys Ser Asn Glu Met Phe Ser Lys
 1 5 10 15

MBI0058CIP.ST25.txt

Leu Pro His His Gln Gln Gln Gln Gln Gln Gln Gln Gln His Ser
 20 25 30

Leu Thr Ser His Phe His Leu Ser Ser Thr Val Thr Pro Thr Val Asp
 35 40 45

Asp Ser Ser Ile Glu Val Val Arg Arg Pro Arg Gly Arg Pro Pro Gly
 50 55 60

Ser Lys Asn Lys Pro Lys Pro Pro Val Phe Val Thr Arg Asp Thr Asp
 65 70 75 80

Pro Pro Met Ser Pro Tyr Ile Leu Glu Val Pro Ser Gly Asn Asp Val
 85 90 95

Val Glu Ala Ile Asn Arg Phe Cys Arg Arg Lys Ser Ile Gly Val Cys
 100 105 110

Val Leu Ser Gly Ser Gly Ser Val Ala Asn Val Thr Leu Arg Gln Pro
 115 120 125

Ser Pro Ala Ala Leu Gly Ser Thr Ile Thr Phe His Gly Lys Phe Asp
 130 135 140

Leu Leu Ser Val Ser Ala Thr Phe Leu Pro Pro Pro Pro Arg Thr Ser
 145 150 155 160

Leu Ser Pro Pro Val Ser Asn Phe Phe Thr Val Ser Leu Ala Gly Pro
 165 170 175

Gln Gly Gln Ile Ile Gly Gly Phe Val Ala Gly Pro Leu Ile Ser Ala
 180 185 190

Gly Thr Val Tyr Val Ile Ala Ala Ser Phe Asn Asn Pro Ser Tyr His
 195 200 205

Arg Leu Pro Ala Glu Glu Glu Gln Lys His Ser Ala Gly Thr Gly Glu
 210 215 220

Arg Glu Gly Gln Ser Pro Pro Val Ser Gly Gly Gly Glu Glu Ser Gly
 225 230 235 240

Gln Met Ala Gly Ser Gly Gly Glu Ser Cys Gly Val Ser Met Tyr Ser
 245 250 255

Cys His Met Gly Gly Ser Asp Val Ile Trp Ala Pro Thr Ala Arg Ala
 260 265 270

Pro Pro Pro Tyr
275

<210> 317
<211> 1050
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G2155 Functionally related and homologous to G1073

<400> 317
ctcatatata ccaaccaaac ctctctctgc atctttatta acacaaaatt ccaaaagatt 60
aaatggtgtc gaagctccct acacagcgac acttgacact ctctccctcc tctccctcca 120
tggaaccgt cggggtcca cgtggcagac ctcgagggtc caaaaacaaa cctaaagctc 180
caatctttgt caccattgac cctcctatga gtccttacat cctcgaagtg ccacccggaa 240
acgatgtcgt tgaagcccta aaccgtttct gccgcggtaa agccatcggc ttttgcgctc 300
tcagtggctc aggtccgtt gctgatgtca ctttgcgta gccttctccg gcagctcctg 360
gctcaaccat tactttccac ggaaagttcg atcttctctc tgtctccgcc actttcctcc 420
ctcctctacc tcctacctcc ttgtccctc ccgtctccaa tttcttcacc gtctctctcg 480
ccggacctca ggggaaagtc atcgggtgat tcgtcgtgg tcctctcggt gccgccggaa 540
ctgtttactt cgtcgccact agtttcaaga acccttctta tcaccgggta cctgctacgg 600
aggaagagca aagaaactcg gcggaagggg aagaggaggg acaatcgccg ccggtctctg 660
gaggtggtgg agagtcgatg tacgtgggtg gctctgatgt catttgggat cccaacgcca 720
aagctccatc gccgtactga ccacaaatcc atctcggtta aactagggtt tcttcttctt 780
tagatcatca agaatcaaca aaaagattgc attttttagat tctttgtaat atcataattg 840
actcactctt taatctctct atcacttctt ctttagcttt ttctgcagtg tcaaacttca 900
catatttgta gtttgatttg actatcccca agttttgtat tttatcatac aaatttttgc 960
ctgtctctaa tggttgtttt ttcgtttgta taatcttatg cattgtttat tggagctcca 1020
gagattgaat gtataatata atggtttaat 1050

<210> 318
<211> 225
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G2155 polypeptide Functionally related and homologous to G1073

<400> 318

Met Leu Ser Lys Leu Pro Thr Gln Arg His Leu His Leu Ser Pro Ser
1 5 10 15

MBI0058CIP.ST25.txt

Ser Pro Ser Met Glu Thr Val Gly Arg Pro Arg Gly Arg Pro Arg Gly
20 25 30

Ser Lys Asn Lys Pro Lys Ala Pro Ile Phe Val Thr Ile Asp Pro Pro
35 40 45

Met Ser Pro Tyr Ile Leu Glu Val Pro Ser Gly Asn Asp Val Val Glu
50 55 60

Ala Leu Asn Arg Phe Cys Arg Gly Lys Ala Ile Gly Phe Cys Val Leu
65 70 75 80

Ser Gly Ser Gly Ser Val Ala Asp Val Thr Leu Arg Gln Pro Ser Pro
85 90 95

Ala Ala Pro Gly Ser Thr Ile Thr Phe His Gly Lys Phe Asp Leu Leu
100 105 110

Ser Val Ser Ala Thr Phe Leu Pro Pro Leu Pro Pro Thr Ser Leu Ser
115 120 125

Pro Pro Val Ser Asn Phe Phe Thr Val Ser Leu Ala Gly Pro Gln Gly
130 135 140

Lys Val Ile Gly Gly Phe Val Ala Gly Pro Leu Val Ala Ala Gly Thr
145 150 155 160

Val Tyr Phe Val Ala Thr Ser Phe Lys Asn Pro Ser Tyr His Arg Leu
165 170 175

Pro Ala Thr Glu Glu Glu Gln Arg Asn Ser Ala Glu Gly Glu Glu Glu
180 185 190

Gly Gln Ser Pro Pro Val Ser Gly Gly Gly Gly Glu Ser Met Tyr Val
195 200 205

Gly Gly Ser Asp Val Ile Trp Asp Pro Asn Ala Lys Ala Pro Ser Pro
210 215 220

Tyr
225

<210> 319
<211> 1361
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G2156 Predicted polypeptide sequence is paralogous to G1073

MBI0058CIP.ST25.txt

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<400> 319
ttttttttcc ctttcctcgt tcaaaaaaag tacttgacaga gtcaactcact ctcagttctca      60
gcacatgaat taatttgaag cttccctaga attctttcac atcaattaat acgacaccgt      120
ctcgggtgaa gaatctctcc tctcttgccc taaagcgagt tagggtttaa cacacaaagc      180
atacccttta gatttgtgtc tcttagctct gtttttgtcg gcttgtgtaa cccgatcaact      240
caagctattg gctcctcacc tcctgaaatt tgactttctcc aatggatctc aaagtttctc      300
ttatatgaat tctatcttca ccttcacaat atctttatat atatgagcca caagaacaag      360
aagagtcagt agatgcggct gccatggacg gtggttacga tcaatccgga ggagcttcta      420
gatactttca caacctcttc aggcctgagc ttcacaccca gcttcaacct cagcctcaac      480
ttcacccttt gcctcagcct cagcctcaac ctcagcctca gcagcagaat tcagatgatg      540
aatctgactc caacaaggat ccgggttccg acccagttac ctctgggtca accgggaaac      600
gtccacgtgg acgtcctccg ggatccaaga acaagccgaa gccaccgggt atagtgacta      660
gagatagccc caacgtgctt agatctcatg ttcttgaagt ctcatctgga gccgacatag      720
tcgagagcgt taccacttac gctcgcagga gaggaagagg agtctccatt ctcagtggtta      780
acggcacggg ggctaacgtc agtctccggc agccggcaac gacagcggct catggggcaa      840
atggtggaac cggaggtggt gtggctctac atggaagggt tgagatactt tccctcacag      900
gtacgggtgtt gccgccccct gcgccgccag gatccgggtg tctttctatc tttctttccg      960
gcgttcaagg tcaggtgatt ggaggaaacg tgggtggtcc gcttgtggct tcgggtccag     1020
tgatacta at ggctgcatcg ttctcta atg caactttcga aaggcttccc cttgaagatg     1080
aaggaggaga aggtggagag ggaggagaag ttggagaggg aggaggagga gaaggtggtc     1140
caccgccggc cacgtcatca tcaccaccat ctggagccgg tcaaggacag ttaagaggta     1200
acatgagtggt ttatgatcag ttgcccgtg atcctcattt gcttgggttg ggagccgcag     1260
ccgcagccgc accaccaaga ccagcctttt agaattgaaa attatgtccg taacatagct     1320
gtaaccaa at ttcatttctc aaaattaaaa gaaaaaaaaa a                          1361

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<210> 320
<211> 302
<212> PRT
<213> Arabidopsis thaliana

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<220>
<223> G2156 polypeptide Paralogous to G1073

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<400> 320

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Met Asp Gly Gly Tyr Asp Gln Ser Gly Gly Ala Ser Arg Tyr Phe His
1          5          10          15

```

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Asn Leu Phe Arg Pro Glu Leu His His Gln Leu Gln Pro Gln Pro Gln
          20          25          30

```

Leu His Pro Leu Pro Gln Pro Gln Pro Gln Pro Gln Pro Gln Gln Gln
 35 40 45
 Asn Ser Asp Asp Glu Ser Asp Ser Asn Lys Asp Pro Gly Ser Asp Pro
 50 55 60
 Val Thr Ser Gly Ser Thr Gly Lys Arg Pro Arg Gly Arg Pro Pro Gly
 65 70 75 80
 Ser Lys Asn Lys Pro Lys Pro Pro Val Ile Val Thr Arg Asp Ser Pro
 85 90 95
 Asn Val Leu Arg Ser His Val Leu Glu Val Ser Ser Gly Ala Asp Ile
 100 105 110
 Val Glu Ser Val Thr Thr Tyr Ala Arg Arg Arg Gly Arg Gly Val Ser
 115 120 125
 Ile Leu Ser Gly Asn Gly Thr Val Ala Asn Val Ser Leu Arg Gln Pro
 130 135 140
 Ala Thr Thr Ala Ala His Gly Ala Asn Gly Gly Thr Gly Gly Val Val
 145 150 155 160
 Ala Leu His Gly Arg Phe Glu Ile Leu Ser Leu Thr Gly Thr Val Leu
 165 170 175
 Pro Pro Pro Ala Pro Pro Gly Ser Gly Gly Leu Ser Ile Phe Leu Ser
 180 185 190
 Gly Val Gln Gly Gln Val Ile Gly Gly Asn Val Val Ala Pro Leu Val
 195 200 205
 Ala Ser Gly Pro Val Ile Leu Met Ala Ala Ser Phe Ser Asn Ala Thr
 210 215 220
 Phe Glu Arg Leu Pro Leu Glu Asp Glu Gly Gly Glu Gly Gly Glu Gly
 225 230 235 240
 Gly Glu Val Gly Glu Gly Gly Gly Gly Glu Gly Gly Pro Pro Pro Ala
 245 250 255
 Thr Ser Ser Ser Pro Pro Ser Gly Ala Gly Gln Gly Gln Leu Arg Gly
 260 265 270
 Asn Met Ser Gly Tyr Asp Gln Phe Ala Gly Asp Pro His Leu Leu Gly
 275 280 285

Trp Gly Ala Ala Ala Ala Ala Ala Pro Pro Arg Pro Ala Phe
 290 295 300

<210> 321
 <211> 813
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <223> G2345 Predicted polypeptide sequence is paralogous to G481 and G482

<400> 321
 cttctccagc gtcggatcag atcagatcaa atctctctct ccatctccgt ctctctctcc 60
 aatcatcatt tctctctccg tctcccgtc tttttcgaat tctccttctt cttcagggtt 120
 tctgagatgg ccgaatcgca aaccgggtgg ggtgggtggg gaagccatga gaggggcggt 180
 gatcagagcc cgaggtcttt gaatgttcgt gagcaggaca ggtttcttcc gattgctaac 240
 ataagccgta tcatgaagag aggtttacct ctaaatggca aaatcgctaa agatgctaaa 300
 gagactatgc aggaatgtgt ctctgaattc atcagcttcg tcaccagcga ggctagtgat 360
 aagtgcacaa gagagaaaag gaagaccatc aatggagatg atttgctttg ggctatggcc 420
 actttaggat tcgaagatta catcgatccc ctcaagggtt acctgatgcg atatagagag 480
 atggaggggtg aactaaagg atcaggaaaa ggcggggaat cgagtgcacaa gagagatggg 540
 caaccaagcc aagtgtctca gttctcgcag gttcctcaac aaggctcatt ctcacagggt 600
 ccttatggaa actctcaatc tctgaggttc ggcaatagca tcgagcatct tgaagtgtta 660
 atgagtagta ctaggacact attcatcaca atcttccgag actcgactat gcctgttggtg 720
 tctgagaatc tgagtgatcc actttccata gatatggatt gtgaagctat ttatcaccac 780
 ttcattggcc tgttgattct ttcatgcaag tga 813

<210> 322
 <211> 228
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> G2345 polypeptide Paralogous to G481 and G482

<400> 322

Met Ala Glu Ser Gln Thr Gly Gly Gly Gly Gly Gly Ser His Glu Ser
 1 5 10 15

Gly Gly Asp Gln Ser Pro Arg Ser Leu Asn Val Arg Glu Gln Asp Arg
 20 25 30

Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Arg Gly Leu Pro
 35 40 45

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Leu Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu Thr Met Gln Glu Cys
50 55 60

Val Ser Glu Phe Ile Ser Phe Val Thr Ser Glu Ala Ser Asp Lys Cys
65 70 75 80

Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala
85 90 95

Met Ala Thr Leu Gly Phe Glu Asp Tyr Ile Asp Pro Leu Lys Val Tyr
100 105 110

Leu Met Arg Tyr Arg Glu Met Glu Gly Asp Thr Lys Gly Ser Gly Lys
115 120 125

Gly Gly Glu Ser Ser Ala Lys Arg Asp Gly Gln Pro Ser Gln Val Ser
130 135 140

Gln Phe Ser Gln Val Pro Gln Gln Gly Ser Phe Ser Gln Gly Pro Tyr
145 150 155 160

Gly Asn Ser Gln Ser Leu Arg Phe Gly Asn Ser Ile Glu His Leu Glu
165 170 175

Val Leu Met Ser Ser Thr Arg Thr Leu Phe Ile Thr Ile Phe Arg Asp
180 185 190

Ser Thr Met Pro Val Val Ser Glu Asn Leu Ser Asp Pro Leu Ser Ile
195 200 205

Asp Met Asp Cys Glu Ala Ile Tyr His His Phe Ile Gly Leu Leu Ile
210 215 220

Leu Ser Cys Lys
225

<210> 323

<211> 1424

<212> DNA

<213> Arabidopsis thaliana

<220>

<223> G2657 Functionally related and homologous to G1073

<400> 323

gaaaataaaa ccttaccaaa tcaatcaaag aataagatga agaacaaaat tccagcttga 60

tgtattttgt gaaaacatta ttattctttt cctcttctat ctagagtctc tcctaggtca 120

aattatcaaa atcaattctc atctcaacat agaatggatc cagttcaatc tcatggatca 180

MBI0058CIP.ST25.txt

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caaagctctc ttcctcctcc ttcccatgct agagatttcc aattacatct tcaacaacaa 240
caacaacatc aacaacaaca tcaacaacaa caacaacaac agttctttct ccaccatcat 300
cagcaaccac aaagaaacct tgatcaagat cagcagcagc aaggagggtc aatattgaat 360
agatctatca agatggatcg cgaagagaca agcgataaca tggacaacat cgctaatacc 420
aacagcggta gcgaaggtaa agagatgagt ttacacggag gagaaggagg aagcggtggt 480
ggaggaagtg gagaacagat gacaagaagg ccaagaggaa gaccagcagg atccaagaac 540
aaacctaaag ctccaataat cataacaaga gacagcgcaa acgcgcttcg aactcacgtc 600
atggagatag gagacggatg tgacatagtt gactgtatgg ctacgttcgc tagacgccgc 660
caaagaggcg tttgcgttat gagcggtaga ggaagcgtaa ctaacgtcac tatacgtcag 720
cctggatcgc cacctggctc ggtggttagc cttcacggcc ggtttgaaat cctctctctt 780
tcgggatctt tcttgccctc gcctgcgccg cctgcagcca ccggactaag cgtttaccta 840
gccggaggac aagggcaggt cgttggaggt agtgtggtgg gacctttgtt gtgttcgggt 900
cctgtggtgg ttatggcggc ttcttttagc aatgcggcgt acgaaaggct gcctttggaa 960
gaagatgaga tgcagacgcc agttcaagga ggcggtggag gaggaggagg tgggtggtgga 1020
atgggatctc ccccgatgat gggacagcaa caagctatgg cagctatggc ggcggtcaa 1080
ggactaccac cgaatcttct tggttcggtt cagttgccac cgccacaaca gaatgatcag 1140
cagtattggt ctacgggtcg gccaccgat tgattattag attgctatta ttatatatac 1200
atgatcaatg gaatatatac atatatagct atgtatttgt atatatgtag ctatttacta 1260
atagatctta catatatata aagcaagcta acatggaatc attaaaagga ggtctacgaa 1320
gtatgacgtg aagttgaaga cggcgataat attgaagatc aacaattcag tagatggttt 1380
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<210> 324

<211> 339

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G2657 polypeptide Functionally related and homologous to G1073

<400> 324

Met Asp Pro Val Gln Ser His Gly Ser Gln Ser Ser Leu Pro Pro Pro
1 5 10 15

Phe His Ala Arg Asp Phe Gln Leu His Leu Gln Gln Gln Gln Gln His
20 25 30

Gln Gln Gln His Gln Gln Gln Gln Gln Gln Gln Phe Phe Leu His His
35 40 45

His Gln Gln Pro Gln Arg Asn Leu Asp Gln Asp His Glu Gln Gln Gly
 50 55 60
 Gly Ser Ile Leu Asn Arg Ser Ile Lys Met Asp Arg Glu Glu Thr Ser
 65 70 75 80
 Asp Asn Met Asp Asn Ile Ala Asn Thr Asn Ser Gly Ser Glu Gly Lys
 85 90 95
 Glu Met Ser Leu His Gly Gly Glu Gly Gly Ser Gly Gly Gly Gly Ser
 100 105 110
 Gly Glu Gln Met Thr Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys
 115 120 125
 Asn Lys Pro Lys Ala Pro Ile Ile Ile Thr Arg Asp Ser Ala Asn Ala
 130 135 140
 Leu Arg Thr His Val Met Glu Ile Gly Asp Gly Cys Asp Ile Val Asp
 145 150 155 160
 Cys Met Ala Thr Phe Ala Arg Arg Arg Gln Arg Gly Val Cys Val Met
 165 170 175
 Ser Gly Thr Gly Ser Val Thr Asn Val Thr Ile Arg Gln Pro Gly Ser
 180 185 190
 Pro Pro Gly Ser Val Val Ser Leu His Gly Arg Phe Glu Ile Leu Ser
 195 200 205
 Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala Pro Pro Ala Ala Thr Gly
 210 215 220
 Leu Ser Val Tyr Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly Ser
 225 230 235 240
 Val Val Gly Pro Leu Leu Cys Ser Gly Pro Val Val Val Met Ala Ala
 245 250 255
 Ser Phe Ser Asn Ala Ala Tyr Glu Arg Leu Pro Leu Glu Glu Asp Glu
 260 265 270
 Met Gln Thr Pro Val Gln Gly Gly Gly Gly Gly Gly Gly Gly Gly
 275 280 285
 Gly Met Gly Ser Pro Pro Met Met Gly Gln Gln Gln Ala Met Ala Ala
 290 295 300

Met Ala Ala Ala Gln Gly Leu Pro Pro Asn Leu Leu Gly Ser Val Gln
305 310 315 320

Leu Pro Pro Pro Gln Gln Asn Asp Gln Gln Tyr Trp Ser Thr Gly Arg
325 330 335

Pro Pro Tyr

<210> 325
<211> 252
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> G2718 Predicted polypeptide sequence is paralogous to G481 and G482

<400> 325
atgaatacgc agcgtaagtc gaagcatctt aagaccaatc caaccattgt tgcctcttct 60
tctgaagaag tgagcagtct tgagtgggaa gaaatagcaa tggctcagga agaagaggat 120
ttgatttgca ggatgtataa gcttgctcggg gaaaggtggg atttaatagc` tgggaggatt 180
ccaggaagaa cagcagaaga gattgagagg ttttgggtga tgaagaatca tcgaagatct 240
caattacgtt ga 252

<210> 326
<211> 83
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G2718 polypeptide Paralogous to G481 and G482

<400> 326

Met Asn Thr Gln Arg Lys Ser Lys His Leu Lys Thr Asn Pro Thr Ile
1 5 10 15

Val Ala Ser Ser Ser Glu Glu Val Ser Ser Leu Glu Trp Glu Glu Ile
20 25 30

Ala Met Ala Gln Glu Glu Glu Asp Leu Ile Cys Arg Met Tyr Lys Leu
35 40 45

Val Gly Glu Arg Trp Asp Leu Ile Ala Gly Arg Ile Pro Gly Arg Thr
50 55 60

Ala Glu Glu Ile Glu Arg Phe Trp Val Met Lys Asn His Arg Arg Ser
65 70 75 80

Gln Leu Arg

<210> 327
 <211> 321
 <212> DNA
 <213> Oryza sativa (japonica cultivar-group)

<220>
 <223> G3392 Predicted polypeptide sequence is orthologous to G682

<400> 327
 gctctaaact accataaaat cttactcgg cattttttttt ttcacgctaa tggaaagtag 60
 cgggtggaagc cagctgggaa agaattccaa aacaagtgat ggctcgtgaaa caaaagaagt 120
 taatagcact gcgcaaaatt ttgttcattt cacagaagaa gaggaagata ttgttttcag 180
 aatgcacagg cttgtcggga acaggtggga acttatagct ggaagaatac cgggaaggac 240
 agcagaagaa gtagagaagt tctgggcaat taaacatcaa gccacatgat agcagaaaga 300
 ggatgtttgc cccaaaagta g 321

<210> 328
 <211> 79
 <212> PRT
 <213> Oryza sativa (japonica cultivar-group)

<220>
 <223> G3392 polypeptide Orthologous to G682

<400> 328

Met Glu Ser Ser Gly Gly Ser Gln Leu Gly Lys Asn Ser Lys Thr Ser
 1 5 10 15

Asp Gly Arg Glu Thr Lys Glu Val Asn Ser Thr Ala Gln Asn Phe Val
 20 25 30

His Phe Thr Glu Glu Glu Asp Ile Val Phe Arg Met His Arg Leu
 35 40 45

Val Gly Asn Arg Trp Glu Leu Ile Ala Gly Arg Ile Pro Gly Arg Thr
 50 55 60

Ala Glu Glu Val Glu Lys Phe Trp Ala Ile Lys His Gln Ala Thr
 65 70 75

<210> 329
 <211> 356
 <212> DNA
 <213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3393 Predicted polypeptide sequence is orthologous to G682

<400> 329
cataaggtca taacaagggc ctgaggatct tagctagcac aagatctcaa ctcggcattt 60
cattggagtt tttcacgcct aatggatagc agcagtggta gccagggaaa gaattccaaa 120
accagtgatg gttgtgaaac aaaagaagtt aataacactg cacagaattt tgttcatttc 180
acggaagaag aggaagatct cgttttcaga atgcacaggc ttgttgggaa caggtgggaa 240
cttatagctg gaagaatccc tggaagaaca gcaaaagagg tagaaatgtt ctgggcagta 300
aagcaccaga atacataagg ggggaaaaag ggtgtatgcc ctaaaagtag cgtaca 356

<210> 330

<211> 78

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3393 polypeptide Orthologous to G682

<400> 330

Met Asp Ser Ser Ser Gly Ser Gln Gly Lys Asn Ser Lys Thr Ser Asp
1 5 10 15

Gly Cys Glu Thr Lys Glu Val Asn Asn Thr Ala Gln Asn Phe Val His
20 25 30

Phe Thr Glu Glu Glu Glu Asp Leu Val Phe Arg Met His Arg Leu Val
35 40 45

Gly Asn Arg Trp Glu Leu Ile Ala Gly Arg Ile Pro Gly Arg Thr Ala
50 55 60

Lys Glu Val Glu Met Phe Trp Ala Val Lys His Gln Asn Thr
65 70 75

<210> 331

<211> 1231

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3394 Predicted polypeptide sequence is orthologous to G481 and G482

<400> 331
ggccgcttct cttctccagc gtccgatctc cccctctcgc ctctccgcct cacctccgct 60
ccgcttccca cccccgcttc ctctctctct cctctccccc cccctctctc tctctctctc 120
tctctctctc tctctctcgc ttcaccacct cgcgcccac cccctctctc ctctcttcca 180
cgctcgcgccc tctccgcgcg cgcccgcgct tctatataag gaggggggag gtgggatggc 240

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ggatgggccc gggagcccgg ggggaggagg ggggagccac gagagcggga gcccgagggg 300
gggagggggga ggaggggggag gtgggggttg ggggggcccc ctcgtccggc aggacaggtt 360
cctccccatc gccaacatca gccgcatcat gaagaaggcc atcccggcca acgggaagat 420
cgccaaggac gccaaaggaga ccgtgcagga gtgcgtctcc gagttcatct cttcatcac 480
cagcgaggcg agcgataaat gccagaggga gaagcgcaag accatcaacg gcgacgactt 540
gctgtgggcg atggccacgc tgggcttcga ggactacatc gagcccctca aggtctacct 600
gcagaagtac agagagatgg agggatgatag taaattaact gcaaaggctg gtgatggctc 660
tgtgaaaaag gatgtacttg gttctcatgg aggaagcagt tcaagtgcc aagggatggg 720
ccaacaagca gcatacaatc aaggaatggg ttatatgcaa cctcagtacc ataatgggga 780
tgtctcaaac tgaagatagg accttttcat gcaactgttg ctaggtggat tttatttggt 840
gctgcagtcg ttagctaata tatataccta cacctcatgg tgagcagtga aggaagtaac 900
ttgctaccac ctctaggtcc catgtttgtc aaccaggaac tgatgctgct tggaagcgtc 960
gagccaaggc tgcttctcag atgtaaatta ctccccgtga ggatagtttc ggttcgtggg 1020
ctagctctgt tgttgtatgt atattcagga taatttaaca attgggtctt ggctgtcatt 1080
cggttccata taatctgtat tgggaggcat aaatattcat gttgtatttc gtcctgaact 1140
agcgtgttgt actattgaga aatagatgct ctctgtaatg gtagcaattt tactctgatt 1200
ccccaaaaaa aaaaaaaaaa aaaaaaaaaa a 1231

```

<210> 332

<211> 185

<212> PRT

<213> *Oryza sativa* (japonica cultivar-group)

<220>

<223> G3394 polypeptide Orthologous to G481 and G482

<400> 332

```

Met Ala Asp Gly Pro Gly Ser Pro Gly Gly Gly Gly Gly Ser His Glu
1           5           10          15

```

```

Ser Gly Ser Pro Arg Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
20          25          30

```

```

Gly Gly Pro Leu Val Arg Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile
35          40          45

```

```

Ser Arg Ile Met Lys Lys Ala Ile Pro Ala Asn Gly Lys Ile Ala Lys
50          55          60

```

```

Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe
65          70          75          80

```

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Ile Thr Ser Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr
85 90 95

Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu
100 105 110

Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu Gln Lys Tyr Arg Glu Met
115 120 125

Glu Gly Asp Ser Lys Leu Thr Ala Lys Ala Gly Asp Gly Ser Val Lys
130 135 140

Lys Asp Val Leu Gly Ser His Gly Gly Ser Ser Ser Ser Ala Gln Gly
145 150 155 160

Met Gly Gln Gln Ala Ala Tyr Asn Gln Gly Met Gly Tyr Met Gln Pro
165 170 175

Gln Tyr His Asn Gly Asp Val Ser Asn
180 185

<210> 333

<211> 610

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3395 Predicted polypeptide sequence is orthologous to G481 and G482

<400> 333

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tggatctagg gtttttggag ggcggcgcg g gatggcgga cgcggggcac gacgagagcg      60
ggagccccgcc gaggagcggc ggggtgaggg agcaggacag gttcctgccc atcgccaaca      120
tcagccgcat catgaagaag gccgtcccgg cgaacggcaa gatcgccaag gacgccaagg      180
agaccctgca ggagtgcgtc tcggagttca tctccttcgt caccagcgag gcgagcgaca      240
aatgtcagaa ggagaagcgc aagaccatca acggggaaga tctcctcttt gcgatgggta      300
cgcttggtctt tgaggagtac gttgatccgt tgaagatcta ttacacaag tacagagaga      360
tggaggggtga tagtaagctg tcctcaaagg ctggtgatgg ttcagtaaag aaggatacaa      420
ttgggtccgca cagtggcgct agtagctcaa gtgcgcaagg gatgggttggg gcttacaccc      480
aaggggatggg ttatatgcaa cctcagtatc ataatgggga cacctaaaga tgaggatagt      540
gaaaattttc agtaactggg gtcctctgtg agttattatc catctgttaa ggaagaaccc      600
acattagggc                                     610
```

<210> 334

<211> 164

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3395 polypeptide Orthologous to G481 and G482

<400> 334

Met Ala Asp Ala Gly His Asp Glu Ser Gly Ser Pro Pro Arg Ser Gly
1 5 10 15

Gly Val Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg
20 25 30

Ile Met Lys Lys Ala Val Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala
35 40 45

Lys Glu Thr Leu Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr
50 55 60

Ser Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Ile Asn
65 70 75 80

Gly Glu Asp Leu Leu Phe Ala Met Gly Thr Leu Gly Phe Glu Glu Tyr
85 90 95

Val Asp Pro Leu Lys Ile Tyr Leu His Lys Tyr Arg Glu Met Glu Gly
100 105 110

Asp Ser Lys Leu Ser Ser Lys Ala Gly Asp Gly Ser Val Lys Lys Asp
115 120 125

Thr Ile Gly Pro His Ser Gly Ala Ser Ser Ser Ser Ala Gln Gly Met
130 135 140

Val Gly Ala Tyr Thr Gln Gly Met Gly Tyr Met Gln Pro Gln Tyr His
145 150 155 160

Asn Gly Asp Thr

<210> 335

<211> 837

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3396 Predicted polypeptide sequence is orthologous to G481 and G482

<400> 335

gtcagatcc ggcgccggt ggcgtctcc tccctctccc tectcccaa ccaacggcgc 60

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```

tgateccctc cgccatctcc gtccatctcc gcctaaaaaa actaagcgat gtcggagggg 120
ttcgacggga cggagaacgg cggcggcggc ggcggaggcg gagtagggaa ggagcaggac 180
cggttcctgc cgatcgccaa catcgggcgc atcatgcgcc gggccgtgcc ggagaacggc 240
aagatcgcca aggactccaa ggagtccgtc caggagtgcg tctccgagtt catcagcttc 300
atcaccagcg aagcaagcga caagtgcctc aaggagaagc gcaagaccat caatggggac 360
gacctgatct ggtcaatggg cacgctcgga ttcgaggact atgtcgagcc tctcaagctc 420
tacctcaggc tctaccggga gacggagggt gacacaaagg gttcaagagc ttctgaactg 480
ccagtaaaga aagatgttgt acttaatgga gatcctggat catcgtttga aggcattag 540
gacgaggagt gtgatagcat ctaggaagga gaaccatcgt ttttagggaa agaacgctcc 600
agcatcctgt tatgttgtaa gcaggatgct tctaaagttc caataccttg ttaccacgaa 660
tgtagtcgt cgttcttttt gaaatgttct tgtgttagcc aggatgtcca aatttgttgt 720
aggttctagt tcagtcgtgt gttgtgtggt tgtgtctaac catatttggc cgtttccggc 780
tgtctgcat atgctaaatt cagaggggta aagagatcta agaaaaaaaa aaaaaaa 837

```

<210> 336

<211> 143

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3396 polypeptide Orthologous to G481 and G482

<400> 336

```

Met Ser Glu Gly Phe Asp Gly Thr Glu Asn Gly Gly Gly Gly Gly Gly
1           5           10           15

```

```

Gly Gly Val Gly Lys Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile
          20           25           30

```

```

Gly Arg Ile Met Arg Arg Ala Val Pro Glu Asn Gly Lys Ile Ala Lys
          35           40           45

```

```

Asp Ser Lys Glu Ser Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe
50           55           60

```

```

Ile Thr Ser Glu Ala Ser Asp Lys Cys Leu Lys Glu Lys Arg Lys Thr
65           70           75           80

```

```

Ile Asn Gly Asp Asp Leu Ile Trp Ser Met Gly Thr Leu Gly Phe Glu
          85           90           95

```

```

Asp Tyr Val Glu Pro Leu Lys Leu Tyr Leu Arg Leu Tyr Arg Glu Thr
          100          105          110

```


Glu Gly Asp Thr Lys Gly Ser Arg Ala Ser Glu Leu Pro Val Lys Lys
115 120 125

Asp Val Val Leu Asn Gly Asp Pro Gly Ser Ser Phe Glu Gly Met
130 135 140

<210> 337

<211> 720

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3397 Predicted polypeptide sequence is orthologous to G481 and G482

<400> 337

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gcgtctgatt tgctgaagag gaggaggagg atgccggact cggacaacga ctccggcggg      60
ccgagcaact acgcgggagg ggagctgtcg tcgccgcggg agcaggacag gttcctgccc      120
atcgcgaaac tgagcaggat catgaagaag gcgctgccgg cgaacgcaa gatcagcaag      180
gacgccaagg agacggtgca ggagtgcgtc tccgagttca tctccttcat caccggcgag      240
gcctccgaca agtgccagcg cgagaagcgc aagaccatca acggcgacga cctgctctgg      300
gccatgacca ccctcggctt cgaggactac gtcgaccccc tcaagcacta cctccacaag      360
ttccgcgaga tcgagggcga gcgcgccgcc gcctccacca ccggcgccgg caccagcgcc      420
gcctccacca cgccgccgca gcagcagcac accgccaatg ccgccggcgg ctacgccggg      480
tacgccgccc cgggagccgg ccccggcggc atgatgatga tgatggggca gccatgtac      540
ggctcgccgc caccgccgcc acagcagcag cagcagcaac accaccacat ggcaatggga      600
ggaagaggcg gcttcggtca tcatcccgcc ggcgggcgcg gcgggtcgtc gtcgtcgtcg      660
gggcacggtc ggcaaaacag gggcgcttga catcgctccg agacgagtag catgcacat      720
```

<210> 338

<211> 219

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3397 polypeptide Orthologous to G481 and G482

<400> 338

Met Pro Asp Ser Asp Asn Asp Ser Gly Gly Pro Ser Asn Tyr Ala Gly
1 5 10 15

Gly Glu Leu Ser Ser Pro Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala
20 25 30

Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile
35 40 45

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Ser Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile
50 55 60

Ser Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg
65 70 75 80

Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly
85 90 95

Phe Glu Asp Tyr Val Asp Pro Leu Lys His Tyr Leu His Lys Phe Arg
100 105 110

Glu Ile Glu Gly Glu Arg Ala Ala Ala Ser Thr Thr Gly Ala Gly Thr
115 120 125

Ser Ala Ala Ser Thr Thr Pro Pro Gln Gln Gln His Thr Ala Asn Ala
130 135 140

Ala Gly Gly Tyr Ala Gly Tyr Ala Ala Pro Gly Ala Gly Pro Gly Gly
145 150 155 160

Met Met Met Met Met Gly Gln Pro Met Tyr Gly Ser Pro Pro Pro Pro
165 170 175

Pro Gln Gln Gln Gln Gln Gln His His His Met Ala Met Gly Gly Arg
180 185 190

Gly Gly Phe Gly His His Pro Gly Gly Gly Gly Gly Gly Ser Ser Ser
195 200 205

Ser Ser Gly His Gly Arg Gln Asn Arg Gly Ala
210 215

<210> 339

<211> 761

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3398 Predicted polypeptide sequence is orthologous to G481 and G482

<400> 339

cctctcctct tcgtcttctt cctcgccttc gcttcgactg cttcgatcga gggagatcga 60

ggttgcatg ccggattcgg acaacgagtc agggggggccg agcaacgcgg gggagtacgc 120

gtcggcgagg gagcaggaca ggttcctgcc gatcgcaaac gtgagcagga tcatgaagag 180

ggcgctcccg gcgaacgcca agatcagcaa ggacgccaaag gagacggtgc aggagtgcgt 240

ctcggagttc atctccttca tcaccggcga ggcctccgac aagtgccagc gggagaagcg 300

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```

caagaccatc aacggcgacg acctcctctg ggcgatgacc acgctcggct tgcaggacta 360
catcgacccg ctcaagctct acctccacaa gttccgcgag ctcgagggcg agaaggccat 420
cggcgccgcc ggcagcggcg gcggtggcgc cgctcctcc ggcggtccg gctccggctc 480
cggctcgcac caccaccagg atgcttcccg gaacaatggc ggatacggca tgtacggcgg 540
cggcggcggc atgatcatga tgatgggaca gcctatgtac ggctcgccgc cggcgctcgtc 600
agctgggtac gcgcagccgc cgccgccccca ccaccaccac caccagatgg tgatgggagg 660
gaaaggtgcg tatggccatg gcggcggcgg cggcggcggg ccctccccgt cgtcgggata 720
cggccggcaa gacaggctat gagcttgctt tcttggttg t 761

```

<210> 340

<211> 224

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3398 polypeptide Orthologous to G481 and G482

<400> 340

Met Pro Asp Ser Asp Asn Glu Ser Gly Gly Pro Ser Asn Ala Gly Glu
1 5 10 15

Tyr Ala Ser Ala Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Val
20 25 30

Ser Arg Ile Met Lys Arg Ala Leu Pro Ala Asn Ala Lys Ile Ser Lys
35 40 45

Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe
50 55 60

Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr
65 70 75 80

Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe Glu
85 90 95

Asp Tyr Ile Asp Pro Leu Lys Leu Tyr Leu His Lys Phe Arg Glu Leu
100 105 110

Glu Gly Glu Lys Ala Ile Gly Ala Ala Gly Ser Gly Gly Gly Ala
115 120 125

Ala Ser Ser Gly Gly Ser Gly Ser Gly Ser Gly Ser His His His Gln
130 135 140

Asp Ala Ser Arg Asn Asn Gly Gly Tyr Gly Met Tyr Gly Gly Gly Gly

145 150 155 160

Gly Met Ile Met Met Met Gly Gln Pro Met Tyr Gly Ser Pro Pro Ala
165 170 175

Ser Ser Ala Gly Tyr Ala Gln Pro Pro Pro Pro His His His His His
180 185 190

Gln Met Val Met Gly Gly Lys Gly Ala Tyr Gly His Gly Gly Gly Gly
195 200 205

Gly Gly Gly Pro Ser Pro Ser Ser Gly Tyr Gly Arg Gln Asp Arg Leu
210 215 220

<210> 341

<211> 1160

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3399 Predicted polypeptide sequence is orthologous to G1073

<400> 341

cggtgaggag cgagttgtag aggaggaggg gcaccgatca accgggaagc tggcggccgg 60
gaagtgggtgg gagcggccag atgacacggc catggccggg atggaccctg gcgggggcgg 120
cgccggcgcc ggcagctcac ggtacttcca ccatctgctc cgaccgcagc agccgtcgcc 180
gctgtcaccg ctgtcgccga catcccatgt caagatggag cactccaaga tgtcaccga 240
caagagcccc gtggcgagg gagatcacgc gggagggagt ggaagcggcg gcgtcgccgg 300
tgaccaccag ccgtcgctgt cgcccatggt gcccgctgag ggtggcagcg gcagcgccgg 360
cggtagtggc tcgggtgggc cgacgcggcg cccgcgcggg cgcccgccc ggtccaagaa 420
caagccgaag ccgcccacatca tcgtgacgcg cgacagcccc aacgcgctgc actcgcacgt 480
gctcgagggtc gccggcgggc ccgacgtcgt cgactgcgtg gccgagtacg cccgccgccg 540
agggcgcggc gtgtgcgtgc tgagcggcg cggcgcgcgt gtcaacgtgg cgctgcggca 600
gccgggcgcg tcgccgccgg gcagcatggt ggccacgctg cggggccgggt tcgagatcct 660
atctctcacg ggcacggtcc tgccgcctcc cgcgccaccc ggcgcgagcg gcctcacgt 720
gttctctctc ggcggccagg gccaggtgat cggcggcagc gtggtgggccc cgctggtcgc 780
cgcgggggccc gtcgtcctga tggcggcctc attcggaac gccgtgtacg agcggtgcc 840
gctggagggc gaggaagagg aggtcgccgc gcccgccgcc ggaggcgaag cacaagatca 900
agtggcacia tcagctggac ccccagggca gcaaccggcg gcgtcacagt cctccggcgt 960
gacaggaggc gacggcaccg gcggcgccgg tggcatgtcg ctctacaacc tcgccgggaa 1020
tgtgggaggc tatcagctcc ccggagacaa cttcggagggt tggagcggcg ccggcgccgg 1080

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cggagtcagg ccaccgttct gacccatgtc ttagcatcca gttcaaaaaat tctccaaatt 1140
aagaattgcg cagtgcaggc 1160

<210> 342
<211> 336
<212> PRT
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3399 polypeptide Orthologous to G1073

<400> 342

Met Ala Gly Met Asp Pro Gly Gly Gly Gly Ala Gly Ala Gly Ser Ser
1 5 10 15

Arg Tyr Phe His His Leu Leu Arg Pro Gln Gln Pro Ser Pro Leu Ser
20 25 30

Pro Leu Ser Pro Thr Ser His Val Lys Met Glu His Ser Lys Met Ser
35 40 45

Pro Asp Lys Ser Pro Val Gly Glu Gly Asp His Ala Gly Gly Ser Gly
50 55 60

Ser Gly Gly Val Gly Gly Asp His Gln Pro Ser Ser Ser Ala Met Val
65 70 75 80

Pro Val Glu Gly Gly Ser Gly Ser Ala Gly Gly Ser Gly Ser Gly Gly
85 90 95

Pro Thr Arg Arg Pro Arg Gly Arg Pro Pro Gly Ser Lys Asn Lys Pro
100 105 110

Lys Pro Pro Ile Ile Val Thr Arg Asp Ser Pro Asn Ala Leu His Ser
115 120 125

His Val Leu Glu Val Ala Gly Gly Ala Asp Val Val Asp Cys Val Ala
130 135 140

Glu Tyr Ala Arg Arg Arg Gly Arg Gly Val Cys Val Leu Ser Gly Gly
145 150 155 160

Gly Ala Val Val Asn Val Ala Leu Arg Gln Pro Gly Ala Ser Pro Pro
165 170 175

Gly Ser Met Val Ala Thr Leu Arg Gly Arg Phe Glu Ile Leu Ser Leu
180 185 190

Thr Gly Thr Val Leu Pro Pro Pro Ala Pro Pro Gly Ala Ser Gly Leu

195

200

205

Thr Val Phe Leu Ser Gly Gly Gln Gly Gln Val Ile Gly Gly Ser Val
210 215 220

Val Gly Pro Leu Val Ala Ala Gly Pro Val Val Leu Met Ala Ala Ser
225 230 235 240

Phe Ala Asn Ala Val Tyr Glu Arg Leu Pro Leu Glu Gly Glu Glu Glu
245 250 255

Glu Val Ala Ala Pro Ala Ala Gly Gly Glu Ala Gln Asp Gln Val Ala
260 265 270

Gln Ser Ala Gly Pro Pro Gly Gln Gln Pro Ala Ala Ser Gln Ser Ser
275 280 285

Gly Val Thr Gly Gly Asp Gly Thr Gly Gly Ala Gly Gly Met Ser Leu
290 295 300

Tyr Asn Leu Ala Gly Asn Val Gly Gly Tyr Gln Leu Pro Gly Asp Asn
305 310 315 320

Phe Gly Gly Trp Ser Gly Ala Gly Ala Gly Gly Val Arg Pro Pro Phe
325 330 335

<210> 343

<211> 1143

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3400 Predicted polypeptide sequence is orthologous to G1073

<400> 343

ctctgcaggt gaggtgaggt gaggggtggg atcgagggat cgagaagctg gcggcgagca 60

agtgggtggga gcgcgccgat gagggcgcca tggccgggat ggatcccacc ggcggcgggtg 120

gcggcgggcgg cgtggcgggcg cactacctac acatgctccg cgcgcagcag caccagccac 180

tgtccccggc aggtgacgtc aaggcggagc ggtccatgct gtcgccggat gagagccccg 240

gcgcggyacgc cgacctagga tcggaccacc cgacgtcgtc ggccatggtg gcggcggagg 300

acagcggcgg cggcagcgggt tcgggtggcc cgatgcggcg ccccgcggg aggccgctgg 360

gctccaagaa caagcccaag ccgcccata tcgtgacgcg ggacagcccc aacgcgttcc 420

actcccacgt cctcgaggtc gccgcgggaa ccgacatcgt cgagtgcgtc tgcgagttcg 480

cgcgcgcggc cggccgcggc gtctccgtgc tcagcgggtg cggcgcggtc gccaacgtcg 540

cgctccgcca gccaggcgcg tcgcccccg gcagcctggt cgccaccatg cgcggccagt 600

MBI0058CIP.ST25.txt

tcgagatcct gtccttcacg ggcaccgtcc tcccgccgcc cgcgccgcc agcgccagcg 660
gcctcaccgt cttcctctcc ggcgggcagg gccagggtggc cggcgggagc gtggccggcc 720
agctcatcgc cgcggggcca gtcttctca tggccgcctc gttcgccaat gccgtctacg 780
agcgtctgcc actcgatggg gaggatccgg aggagaggc tgccgccgcc acccctcccg 840
gcgatgcggc gcagccaacc ggcccaccac caccgcagca gcagcccaca gcctcgcagt 900
cctctgaggt gaccgccggt gacggcgggc gcggcgggcg tctcggcattg tatcttgagg 960
gccatgtggg atcctaccag cagcagcagc agcaacttcc cggaccagga gacaacttcg 1020
gtagctggag cggcagcatc aggcgcgcgc cattctgatc caaacacctc aaatcaagct 1080
ctcccccaac aacgccatgc atgtctaaat cctcacaaga ttactccaa gaagacgaag 1140
ctg 1143

<210> 344

<211> 322

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3400 polypeptide Orthologous to G1073

<400> 344

Met Ala Gly Met Asp Pro Thr Gly Gly Gly Gly Gly Gly Gly Val Ala
1 5 10 15

Ala His Tyr Leu His Met Leu Arg Ala Gln Gln His Gln Pro Leu Ser
20 25 30

Pro Ala Gly Asp Val Lys Ala Glu Arg Ser Met Leu Ser Pro Asp Glu
35 40 45

Ser Pro Gly Ala Asp Ala Asp Leu Gly Ser Asp His Pro Thr Ser Ser
50 55 60

Ala Met Val Ala Ala Glu Asp Ser Gly Gly Gly Ser Gly Ser Gly Gly
65 70 75 80

Pro Met Arg Arg Pro Arg Gly Arg Pro Leu Gly Ser Lys Asn Lys Pro
85 90 95

Lys Pro Pro Ile Ile Val Thr Arg Asp Ser Pro Asn Ala Phe His Ser
100 105 110

His Val Leu Glu Val Ala Ala Gly Thr Asp Ile Val Glu Cys Val Cys
115 120 125

Glu Phe Ala Arg Arg Arg Gly Arg Gly Val Ser Val Leu Ser Gly Gly

```

130                               135                               140

Gly Ala Val Ala Asn Val Ala Leu Arg Gln Pro Gly Ala Ser Pro Pro
145                               150                               155                               160

Gly Ser Leu Val Ala Thr Met Arg Gly Gln Phe Glu Ile Leu Ser Leu
165                               170                               175

Thr Gly Thr Val Leu Pro Pro Pro Ala Pro Pro Ser Ala Ser Gly Leu
180                               185                               190

Thr Val Phe Leu Ser Gly Gly Gln Gly Gln Val Val Gly Gly Ser Val
195                               200                               205

Ala Gly Gln Leu Ile Ala Ala Gly Pro Val Phe Leu Met Ala Ala Ser
210                               215                               220

Phe Ala Asn Ala Val Tyr Glu Arg Leu Pro Leu Asp Gly Glu Asp Pro
225                               230                               235                               240

Glu Ala Glu Ala Ala Ala Thr Pro Pro Gly Asp Ala Ala Gln Pro
245                               250                               255

Thr Gly Pro Pro Pro Pro Gln Gln Gln Pro Thr Ala Ser Gln Ser Ser
260                               265                               270

Glu Val Thr Ala Gly Asp Gly Gly Gly Gly Gly Gly Leu Gly Met Tyr
275                               280                               285

Leu Gly Gly His Val Gly Ser Tyr Gln Gln Gln Gln Gln Gln Leu Pro
290                               295                               300

Gly Pro Gly Asp Asn Phe Gly Ser Trp Ser Gly Ser Ile Arg Pro Pro
305                               310                               315                               320

```

Pro Phe

```

<210> 345
<211> 1003
<212> DNA
<213> Oryza sativa (japonica cultivar-group)

```

```

<220>
<223> G3401 Predicted polypeptide sequence is orthologous to G1073

```

```

<400> 345
ggatatatag gccgcaggta gaagctggcg agccggtggt gggacgaggg gcggctcagc      60
ctgccggtga cagccgccga cccatccctc ggccttggca acaacgacac caccggcgcc      120

```


MBI0058CIP.ST25.txt

ggtgacgacg acatggcgctc caaggagcca agcggcgacc acgaccacga gatgaacggg 180
accagcgccg gggggcggcga gcccaaggac ggcgcggtgg tgaccggccg caaccggcgc 240
ccccgcggac ggccgcccgg ctccaagaac aagcccaagc cgcccatctt cgtgacgcgg 300
gacagcccga acgcgctgcg cagccacgtc atggaggtgg ccggcggcgc cgatgtcgcc 360
gagtccatcg cgcacttcgc gcggcgggcg cagcgcggcg tctgcgtgct cagcggggcc 420
ggcaccgtga ccgacgtggc cctgcgccag ccggccgcgc cgagcgccgt ggtggcgctc 480
cgtggggcgg tgcagatcct gtccctgacg gggacgttcc tgccggggcc ggcgccgcgc 540
ggctccaccg ggctgaccgt gtacctcgcc ggcgggcagg ggcaggtggt gggcggcagc 600
gtggtgggga cgctcaccgc ggcgggggcg gtcattgtga tcgcctccac cttcgccaac 660
gccacctacg agaggctgcc gctggatcag gaggaggagg aagcagcggc aggcggcatg 720
atggcgccgc cgccactcat ggccggcgcc gccgatccac tacttttcgg cgggggaatg 780
cacgacgccg ggcttgctgc atggcaccat gcccgcctc cgccgccgc gccctactag 840
ctctctagct agattaatta attaagcttc atgaattaaa tccttgctta attaattggc 900
atatatatat actcacatga tatatatgat caacaagcta tatatagcta gccagctcga 960
gctaattaat taacaaaagg tgagccaata taatgcaaga tcg 1003

<210> 346

<211> 235

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3401 polypeptide Orthologous to G1073

<400> 346

Met Ala Ser Lys Glu Pro Ser Gly Asp His Asp His Glu Met Asn Gly
1 5 10 15

Thr Ser Ala Gly Gly Gly Glu Pro Lys Asp Gly Ala Val Val Thr Gly
20 25 30

Arg Asn Arg Arg Pro Arg Gly Arg Pro Pro Gly Ser Lys Asn Lys Pro
35 40 45

Lys Pro Pro Ile Phe Val Thr Arg Asp Ser Pro Asn Ala Leu Arg Ser
50 55 60

His Val Met Glu Val Ala Gly Gly Ala Asp Val Ala Glu Ser Ile Ala
65 70 75 80

His Phe Ala Arg Arg Arg Gln Arg Gly Val Cys Val Leu Ser Gly Ala
85 90 95

MBI0058CIP.ST25.txt

Gly Thr Val Thr Asp Val Ala Leu Arg Gln Pro Ala Ala Pro Ser Ala
100 105 110

Val Val Ala Leu Arg Gly Arg Phe Glu Ile Leu Ser Leu Thr Gly Thr
115 120 125

Phe Leu Pro Gly Pro Ala Pro Pro Gly Ser Thr Gly Leu Thr Val Tyr
130 135 140

Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly Ser Val Val Gly Thr
145 150 155 160

Leu Thr Ala Ala Gly Pro Val Met Val Ile Ala Ser Thr Phe Ala Asn
165 170 175

Ala Thr Tyr Glu Arg Leu Pro Leu Asp Gln Glu Glu Glu Glu Ala Ala
180 185 190

Ala Gly Gly Met Met Ala Pro Pro Pro Leu Met Ala Gly Ala Ala Asp
195 200 205

Pro Leu Leu Phe Gly Gly Gly Met His Asp Ala Gly Leu Ala Ala Trp
210 215 220

His His Ala Arg Pro Pro Pro Pro Pro Tyr
225 230 235

<210> 347
<211> 902
<212> DNA
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3403 Predicted polypeptide sequence is orthologous to G1073

<400> 347
tcgaccagtgc cattaattgt gcttctcctg gagcagggtc aagctggcga acaggctcgtg 60
gtgggtcgggc cccatgggct tgccggagca gccgtccggc tcgtcgggccc ccaaggcgga 120
gctccccggtg gccaaaggagc cggaggcgag cccgacgggg ggcgcggcgg cggaccacgc 180
cgacgagaac aacgaatccg gcggcggcga gccgcgggag ggcgccgtgg tggcggcgcc 240
caaccggcgc ccccgcggcc gccgcgggg ctccaagaac aagccgaagc cgcccatctt 300
cgtgacgcgc gacagcccca acgcgtgcg cagccacgtc atggaggtgg ccggcggcgc 360
cgacgtcgcc gacgccatcg cgcagttctc gcgccgccgc cagcgcggcg tctgcgtgct 420
cagcggcgcc gggacggtcg ccaacgtcgc gctgcgccag ccgtcggcgc ccggcgccgt 480
cgtcgccctg cacggccgct tcgagatcct ctccctcacc ggcaccttcc tccccggccc 540

MBI0058CIP.ST25.txt

```

ggcgccctccg ggctccacgg ggctcaccgt ctacctcgcc ggcgggccagg gccaggttgt      600
ggcgggcagc gtcgtgggggt cgctcatcgc cgcggggcccg gtcattggtga tcgcgtccac      660
gttcgccaac gccacctacg agcgccctgcc attggaggaa gaagaggagg gctcaggccc      720
gccccatgccc ggcgggcgccg agccccctcat ggccggcgggc cacggcatcg ccgacccttc      780
ggcgctgcca atgttcaacc tgccgccgag caacgggctc ggcgggcgcg gcgacggttt      840
cccatgggcg gcgcaccccc gccaccgta ctgatcgatg gcaatagcat ggaagattca      900
tt                                                                                   902

```

<210> 348
 <211> 266
 <212> PRT
 <213> Oryza sativa (japonica cultivar-group)

<220>
 <223> G3403 polypeptide Orthologous to G1073

<400> 348

Met Gly Leu Pro Glu Gln Pro Ser Gly Ser Ser Gly Pro Lys Ala Glu
 1 5 10 15

Leu Pro Val Ala Lys Glu Pro Glu Ala Ser Pro Thr Gly Gly Ala Ala
 20 25 30

Ala Asp His Ala Asp Glu Asn Asn Glu Ser Gly Gly Gly Glu Pro Arg
 35 40 45

Glu Gly Ala Val Val Ala Ala Pro Asn Arg Arg Pro Arg Gly Arg Pro
 50 55 60

Pro Gly Ser Lys Asn Lys Pro Lys Pro Pro Ile Phe Val Thr Arg Asp
 65 70 75 80

Ser Pro Asn Ala Leu Arg Ser His Val Met Glu Val Ala Gly Gly Ala
 85 90 95

Asp Val Ala Asp Ala Ile Ala Gln Phe Ser Arg Arg Arg Gln Arg Gly
 100 105 110

Val Cys Val Leu Ser Gly Ala Gly Thr Val Ala Asn Val Ala Leu Arg
 115 120 125

Gln Pro Ser Ala Pro Gly Ala Val Val Ala Leu His Gly Arg Phe Glu
 130 135 140

Ile Leu Ser Leu Thr Gly Thr Phe Leu Pro Gly Pro Ala Pro Pro Gly
 145 150 155 160

MBI0058CIP.ST25.txt

Ser Thr Gly Leu Thr Val Tyr Leu Ala Gly Gly Gln Gly Gln Val Val
165 170 175

Gly Gly Ser Val Val Gly Ser Leu Ile Ala Ala Gly Pro Val Met Val
180 185 190

Ile Ala Ser Thr Phe Ala Asn Ala Thr Tyr Glu Arg Leu Pro Leu Glu
195 200 205

Glu Glu Glu Glu Gly Ser Gly Pro Pro Met Pro Gly Gly Ala Glu Pro
210 215 220

Leu Met Ala Gly Gly His Gly Ile Ala Asp Pro Ser Ala Leu Pro Met
225 230 235 240

Phe Asn Leu Pro Pro Ser Asn Gly Leu Gly Gly Gly Gly Asp Gly Phe
245 250 255

Pro Trp Ala Ala His Pro Arg Pro Pro Tyr
260 265

<210> 349

<211> 1152

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3404 Functionally related and homologous to G1073

<400> 349

accgtgagag agggagacag atggatccgg tgacggcggc ggcggcgcat gggggtgggc	60
accaccacca ccaccacttc ggagcgccac cggtggcggc gttccaccac caccggttcc	120
accacggcgg cggggcgcac taccggcggc cgttcagca gtttcaggag gagcagcagc	180
agcttgtggc ggcggcggcg gcggctggtg ggatggcgaa gcaggagctg gtggatgaga	240
gcaacaacac catcaacagc ggcgggagca acgggagcgg cggggaggag cagaggcagc	300
agtccgggga ggagcagcac cagcaagggg cggcggcgcc ggtggtgatc cggcgtccca	360
ggggccgccc cgccggctcc aagaacaagc ccaagcctcc ggtcatcatc acgcgcgaca	420
gcgccagcgc gctgcgggcg cacgtcctcg aggtcgcctc cgggtgcgac ctcgctcgaca	480
gcgtcgccac gttcgcgcgc cgccgccagg tcggtgtctg cgtgctcagc gccaccggcg	540
ccgtcaccaa cgtctccgtc cggcagcccg gcgcggggccc cggcgccgtc gtcaacctca	600
ccggccgctt cgacatcctc tcgctgtccg gtccttcct cccgccgccc gcgcctcctt	660
ccgccaccgg cctcaccgtc tacgtctccg gcggccaggg gcaggctctg ggcggcacgg	720
tcgccggacc gtcatcgcc gtcggccccg tcgtcatcat ggccgcctcg ttcgggaacg	780

MBI0058CIP.ST25.txt

```
ccgcctacga gcgcctcccg ctcgaggacg acgagccgcc gcagcacatg gcgggcggcg      840
gccagtcctc gccgccgccg ccgccgctgc cattaccacc acaccagcag ccgattcttc      900
aagaccatct gccacacaac ctgatgaacg gaatccacct ccccgggcgac gccgcctacg      960
gctggaccag cggcggcggc ggccggcgcc gcgcggcgcc gtactgatca acatcgatct     1020
cgccggagag aaaaaaaatg gaggagaagg atcggagcga gccgtgcatg gtgtaggatg     1080
aattaagcta agagttaatt tcttcttccg cctttgctaa tcatgatgct ctcgtgttgt     1140
ttaatctgtg gc                                                             1152
```

<210> 350

<211> 328

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3404 polypeptide Functionally related and homologous to G1073

<400> 350

```
Met Asp Pro Val Thr Ala Ala Ala Ala His Gly Gly Gly His His His
1          5          10          15
```

```
His His His Phe Gly Ala Pro Pro Val Ala Ala Phe His His His Pro
20          25          30
```

```
Phe His His Gly Gly Gly Ala His Tyr Pro Ala Ala Phe Gln Gln Phe
35          40          45
```

```
Gln Glu Glu Gln Gln Gln Leu Val Ala Ala Ala Ala Ala Ala Gly Gly
50          55          60
```

```
Met Ala Lys Gln Glu Leu Val Asp Glu Ser Asn Asn Thr Ile Asn Ser
65          70          75          80
```

```
Gly Gly Ser Asn Gly Ser Gly Gly Glu Glu Gln Arg Gln Gln Ser Gly
85          90          95
```

```
Glu Glu Gln His Gln Gln Gly Ala Ala Ala Pro Val Val Ile Arg Arg
100         105         110
```

```
Pro Arg Gly Arg Pro Ala Gly Ser Lys Asn Lys Pro Lys Pro Pro Val
115        120        125
```

```
Ile Ile Thr Arg Asp Ser Ala Ser Ala Leu Arg Ala His Val Leu Glu
130        135        140
```

```
Val Ala Ser Gly Cys Asp Leu Val Asp Ser Val Ala Thr Phe Ala Arg
145        150        155        160
```

MBI0058CIP.ST25.txt

Arg Arg Gln Val Gly Val Cys Val Leu Ser Ala Thr Gly Ala Val Thr
165 170 175

Asn Val Ser Val Arg Gln Pro Gly Ala Gly Pro Gly Ala Val Val Asn
180 185 190

Leu Thr Gly Arg Phe Asp Ile Leu Ser Leu Ser Gly Ser Phe Leu Pro
195 200 205

Pro Pro Ala Pro Pro Ser Ala Thr Gly Leu Thr Val Tyr Val Ser Gly
210 215 220

Gly Gln Gly Gln Val Val Gly Gly Thr Val Ala Gly Pro Leu Ile Ala
225 230 235 240

Val Gly Pro Val Val Ile Met Ala Ala Ser Phe Gly Asn Ala Ala Tyr
245 250 255

Glu Arg Leu Pro Leu Glu Asp Asp Glu Pro Pro Gln His Met Ala Gly
260 265 270

Gly Gly Gln Ser Ser Pro Pro Pro Pro Pro Leu Pro Leu Pro Pro His
275 280 285

Gln Gln Pro Ile Leu Gln Asp His Leu Pro His Asn Leu Met Asn Gly
290 295 300

Ile His Leu Pro Gly Asp Ala Ala Tyr Gly Trp Thr Ser Gly Gly Gly
305 310 315 320

Gly Gly Gly Arg Ala Ala Pro Tyr
325

<210> 351

<211> 1013

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3405 Functionally related and homologous to G1073

<400> 351

ctagctaatt gattgctagc ttgcaaggat ggatccgggtc acggcatcaa tacacgggtca 60

ccatcttcct ccaccgttca acaccgcgga cttccatcac catctccagc agcagcagca 120

ccagctgcat ctcaagaccg aggatgacca aggcggcggtc actccgggtg tcttcggcag 180

ccgcggcacc aagcgcgacc acgacgacga cgagaacagt ggcaacggcc atggaagcgg 240

tggtgacggc ggtgacctcg cgctggtacc cccctcgggt ggccgggccgg acggcgccgg 300

MBI0058CIP.ST25.txt

gagcgagagc gccacgcgcc gcccgagggg acgcccggcg ggggtccaaga acaagccgaa 360
gccaccgatc atcatcacca gggacagcgc caacacgctc cggacgcacg tcatggaggt 420
ggccggcggc tgcgacatct ccgagagcat caccacgttc gcgcgacgcc ggcagcgcg 480
ggtttgctg ctcagcggcg ccggcaccgt cactaacgtc acgctgcggc agcccgcac 540
gcagggagcg gtcgttgccg tccacggccg gtccgagata ctctccctct ccggctcctt 600
cctcccgcgc cccgccccgc cggaggccac ggggctcacc gtctacctgg ccggaggcca 660
gggccagggtc gtgggcggca gcgtcgctcg cgcgctgacc gcggctgggc ctgtggtgat 720
aatggcgcg tcttttgca acgcggtgta cgagcggctg ccgttgagg acgacgagct 780
actggcggt caagggcaag ccgacagcgc tgggttctc gccgcggggc agcaagcggc 840
gcagctcgcc ggcggggccc tccatccaag cctcttccaa ggactaccac caaacctact 900
cggaaacgtg cagctgccgc cggaagccgc ctacggatgg aaccctggag ccggcggtgg 960
ccgcccggcg ccgttctgag atggatcgat tccgcgacag caacgcagca tag 1013

<210> 352

<211> 316

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3405 polypeptide Functionally related and homologous to G1073

<400> 352

Met Asp Pro Val Thr Ala Ser Ile His Gly His His Leu Pro Pro Pro
1 5 10 15

Phe Asn Thr Arg Asp Phe His His His Leu Gln Gln Gln Gln His Gln
20 25 30

Leu His Leu Lys Thr Glu Asp Asp Gln Gly Gly Gly Thr Pro Gly Val
35 40 45

Phe Gly Ser Arg Gly Thr Lys Arg Asp His Asp Asp Asp Glu Asn Ser
50 55 60

Gly Asn Gly His Gly Ser Gly Gly Asp Gly Gly Asp Leu Ala Leu Val
65 70 75 80

Pro Pro Ser Gly Gly Gly Pro Asp Gly Ala Gly Ser Glu Ser Ala Thr
85 90 95

Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys Asn Lys Pro Lys Pro
100 105 110

Pro Ile Ile Ile Thr Arg Asp Ser Ala Asn Thr Leu Arg Thr His Val

115

120

125

Met Glu Val Ala Gly Gly Cys Asp Ile Ser Glu Ser Ile Thr Thr Phe
130 135 140

Ala Arg Arg Arg Gln Arg Gly Val Cys Val Leu Ser Gly Ala Gly Thr
145 150 155 160

Val Thr Asn Val Thr Leu Arg Gln Pro Ala Ser Gln Gly Ala Val Val
165 170 175

Ala Leu His Gly Arg Phe Glu Ile Leu Ser Leu Ser Gly Ser Phe Leu
180 185 190

Pro Pro Pro Ala Pro Pro Glu Ala Thr Gly Leu Thr Val Tyr Leu Ala
195 200 205

Gly Gly Gln Gly Gln Val Val Gly Gly Ser Val Val Gly Ala Leu Thr
210 215 220

Ala Ala Gly Pro Val Val Ile Met Ala Ala Ser Phe Ala Asn Ala Val
225 230 235 240

Tyr Glu Arg Leu Pro Leu Glu Asp Asp Glu Leu Leu Ala Ala Gln Gly
245 250 255

Gln Ala Asp Ser Ala Gly Leu Leu Ala Ala Gly Gln Gln Ala Ala Gln
260 265 270

Leu Ala Gly Gly Ala Val Asp Pro Ser Leu Phe Gln Gly Leu Pro Pro
275 280 285

Asn Leu Leu Gly Asn Val Gln Leu Pro Pro Glu Ala Ala Tyr Gly Trp
290 295 300

Asn Pro Gly Ala Gly Gly Gly Arg Pro Ala Pro Phe
305 310 315

<210> 353

<211> 918

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3406 Functionally related and homologous to G1073

<400> 353

atggcaggctc tcgacctcg caccgccgcg acgcgctacg tccaccagct ccaccacctc 60

caccccgacc tccagctgca gcacagctac gccaaagcagc acgagccgctc cgacgacgac 120

MBI0058CIP.ST25.txt

```

cccaacggca gcggcggcgg cggcaacagc aacggcgggc cgtacgggga ccatgacggc 180
gggtcctcgt cgtcaggtcc tgccaccgac ggcgcggtcg gcgggcccgg cgacgtggtg 240
gcgcgccggc cgcggggggc cccgcctggc tccaagaaca agccgaagcc gccggtgatc 300
atcacgcggg agagcgccaa cacgtgcgc gccacatcc tggaggtcgg gagcggctgc 360
gacgtgttcg agtgcgtctc cacgtacgcg cgccggcggc agcgcggcgt gtgcgtgctg 420
agcggcagcg gcgtggtcac caacgtgacg ctgcgtcagc cgtcggcgcc cgcgggcgcc 480
gtcgtgtcgc tgcacgggag gttcagatc ctgtcgtctt cgggctcctt cctcccgcg 540
ccggctcccc ccggcgccac cagcctcacc atcttcctcg ccgggggcca gggacaggtc 600
gtcggcggca acgtcgtcgg cgcgctctac gccgcgggcc cggtcatcgt catcgcggcg 660
tccttcgcca acgtcgcta cgagcgctc ccaactggagg aggaggaggc gccgccgcg 720
caggccggcc tgcagatgca gcagcccgcc ggcggcgccg atgctggtgg catgggtggc 780
gcgttcccgc cggaccgctc tgccgcggc ctcccgttct tcaacctgcc gctcaacaac 840
atgcccggtg gcggcggctc acagctccct cccggcgccg acggccatgg ctgggcgggc 900
gcacggccac cgttctga 918

```

<210> 354

<211> 305

<212> PRT

<213> *Oryza sativa* (japonica cultivar-group)

<220>

<223> G3406 polypeptide Functionally related and homologous to G1073

<400> 354

```

Met Ala Gly Leu Asp Leu Gly Thr Ala Ala Thr Arg Tyr Val His Gln
1           5           10          15

```

```

Leu His His Leu His Pro Asp Leu Gln Leu Gln His Ser Tyr Ala Lys
          20          25          30

```

```

Gln His Glu Pro Ser Asp Asp Asp Pro Asn Gly Ser Gly Gly Gly Gly
          35          40          45

```

```

Asn Ser Asn Gly Gly Pro Tyr Gly Asp His Asp Gly Gly Ser Ser Ser
          50          55          60

```

```

Ser Gly Pro Ala Thr Asp Gly Ala Val Gly Gly Pro Gly Asp Val Val
65          70          75          80

```

```

Ala Arg Arg Pro Arg Gly Arg Pro Pro Gly Ser Lys Asn Lys Pro Lys
          85          90          95

```

```

Pro Pro Val Ile Ile Thr Arg Glu Ser Ala Asn Thr Leu Arg Ala His

```

```

100                               105                               110
Ile Leu Glu Val Gly Ser Gly Cys Asp Val Phe Glu Cys Val Ser Thr
115                               120                               125

Tyr Ala Arg Arg Arg Gln Arg Gly Val Cys Val Leu Ser Gly Ser Gly
130                               135                               140

Val Val Thr Asn Val Thr Leu Arg Gln Pro Ser Ala Pro Ala Gly Ala
145                               150                               155                               160

Val Val Ser Leu His Gly Arg Phe Glu Ile Leu Ser Leu Ser Gly Ser
165                               170                               175

Phe Leu Pro Pro Pro Ala Pro Pro Gly Ala Thr Ser Leu Thr Ile Phe
180                               185                               190

Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly Asn Val Val Gly Ala
195                               200                               205

Leu Tyr Ala Ala Gly Pro Val Ile Val Ile Ala Ala Ser Phe Ala Asn
210                               215                               220

Val Ala Tyr Glu Arg Leu Pro Leu Glu Glu Glu Glu Ala Pro Pro Pro
225                               230                               235                               240

Gln Ala Gly Leu Gln Met Gln Gln Pro Gly Gly Gly Ala Asp Ala Gly
245                               250                               255

Gly Met Gly Gly Ala Phe Pro Pro Asp Pro Ser Ala Ala Gly Leu Pro
260                               265                               270

Phe Phe Asn Leu Pro Leu Asn Asn Met Pro Gly Gly Gly Gly Ser Gln
275                               280                               285

Leu Pro Pro Gly Ala Asp Gly His Gly Trp Ala Gly Ala Arg Pro Pro
290                               295                               300

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Phe
305

<210> 355
 <211> 987
 <212> DNA
 <213> Oryza sativa (japonica cultivar-group)

<220>
 <223> G3407 Functionally related and homologous to G1073

<400> 355

MBI0058CIP.ST25.txt

tcacatcatcat catcacttgc atatcgaatt attaataata tcgaagatgg caggccttga 60
 tttgggcacc agctacctcc accaccacca atcactgcat ctccgccacg acgatggcgg 120
 cgccggctcc gacgacggcg gccacgacga cctctcgccg gggagcggcg gtggcggcgg 180
 gcccagcagc acggccgggtg gcgcccggat cggcggcggc gaggtcgtcg ctgcccggcc 240
 ccgcccggcg ccgcccgggt ccaagaacaa gcccagccg ccggtgatca tcaccaggga 300
 gagegccaac gcgctcaggg cgcataatct cgaggtagcc gccggttgcg atgtgttcga 360
 ggcgtgacg gcgtacgcgc gccgcccggc gcgcccgggtg tgcgtgctct cggcggcggg 420
 gacagtggcg aacgtcacgc tccggcagcc gcagtcggcg cagcccgggc cggcctcgcc 480
 ggcggtggcg acgctgcacg gcaggttcga gatactctcc ctgcccgggt ccttctgccc 540
 cccgcccgcg ccgcccggcg ccaccagcct cgcgcgttc ctgcccggcg ggcaggggca 600
 ggtcgtcggt ggcagcgtcg ccggcgcgct catcgccggcg gggcccgtcg tcgtcgtcgc 660
 cgcgtcgttc agcaacgtgg cgtacgagag gctgccgctc gaggacggcg acgaggtggt 720
 cccccggcg ccggcagggg gcgaccaggc cggcggcggc agcggcggca tgccaccatt 780
 aggcgttgat ccgtcgggcg gcgcccgcac cggcgggctc ccgttcttca acatgccgtt 840
 cgggatgccg ccaatgccg tggacggcca cgcggctgg cctggcgccg gcgtcgggag 900
 gccaccgttc tcacgatgga tggatcccca tattccggcg agcggccggc ggcgaggtgg 960
 tcggcaagat tgaagacatg gacatgg 987

<210> 356

<211> 289

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3407 polypeptide Functionally related and homologous to G1073

<400> 356

Met Ala Gly Leu Asp Leu Gly Thr Ser Tyr Leu His His His Gln Ser
 1 5 10 15

Leu His Leu Arg His Asp Asp Gly Gly Ala Gly Ser Asp Asp Gly Gly
 20 25 30

His Asp Asp Leu Ser Pro Gly Ser Gly Gly Gly Gly Gly Pro Ser Ser
 35 40 45

Thr Ala Gly Gly Ala Gly Ile Gly Gly Gly Glu Val Val Ala Arg Arg
 50 55 60

Pro Arg Gly Arg Pro Pro Gly Ser Lys Asn Lys Pro Lys Pro Pro Val
 65 70 75 80

MBI0058CIP.ST25.txt

Ile Ile Thr Arg Glu Ser Ala Asn Ala Leu Arg Ala His Ile Leu Glu
85 90 95

Val Ala Ala Gly Cys Asp Val Phe Glu Ala Leu Thr Ala Tyr Ala Arg
100 105 110

Arg Arg Gln Arg Gly Val Cys Val Leu Ser Ala Ala Gly Thr Val Ala
115 120 125

Asn Val Thr Leu Arg Gln Pro Gln Ser Ala Gln Pro Gly Pro Ala Ser
130 135 140

Pro Ala Val Ala Thr Leu His Gly Arg Phe Glu Ile Leu Ser Leu Ala
145 150 155 160

Gly Ser Phe Leu Pro Pro Pro Ala Pro Pro Gly Ala Thr Ser Leu Ala
165 170 175

Ala Phe Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly Ser Val Ala
180 185 190

Gly Ala Leu Ile Ala Ala Gly Pro Val Val Val Val Ala Ala Ser Phe
195 200 205

Ser Asn Val Ala Tyr Glu Arg Leu Pro Leu Glu Asp Gly Asp Glu Val
210 215 220

Val Pro Pro Ala Pro Ala Gly Ser Asp Gln Gly Gly Gly Gly Ser Gly
225 230 235 240

Gly Met Pro Pro Leu Gly Val Asp Pro Ser Gly Gly Ala Ala Thr Gly
245 250 255

Gly Leu Pro Phe Phe Asn Met Pro Phe Gly Met Pro Pro Met Pro Val
260 265 270

Asp Gly His Ala Gly Trp Pro Gly Ala Gly Val Gly Arg Pro Pro Phe
275 280 285

Ser

<210> 357
<211> 1064
<212> DNA
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3408 Functionally related and homologous to G1073
Page 328

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<400> 357
gtgggttttgg ttgattgcta ctctgtgcc a tgctgttctg cgagagggac atgaacaagg      60
agagcatgta ccaagaacgg gacgacatgg cggggatacg gttcgcgacg ccgccgctgc      120
ctcagcagca gcagcagcag cagctgggtg agtgcttctc cgacgaggtg gacagccgcg      180
ggagtggcgg cgagatgaag gatgccgtgg ggagcgggag tgggcagctg gtcgttggtg      240
gtggcgggga tggggcgagc atcgaggtgg cgaagaagag gagggggagg ccgccggggg      300
ccaagaacaa gccgaagcca cccgtgggtg tcacgcggga ggcgagagcc gcggcggcga      360
tgcgcccgca cgtgatcgag atccccggcg ggcgggacgt cgcgaggcg ctcgcgcggt      420
tctcgagccg tcggaacctc gggatctgcg tgctcgccgg caccggcgcg gtcgccaacg      480
tgctgctccg ccacccgtca cccgggggtc cgggctcagc tccggctgcg atcgtgttcc      540
acggccggta cgagatcctc tccctgtcgg ccacgttctc gcctccggcc atgtcctccg      600
tggcgcccca ggccgcggtc gccgcgcggg gcctctccat ctgctcgcc ggcccgcacg      660
gccagatcgt cggcgggggc gtggcaggcc cgctctacgc cgcgaccacc gtcgtggctg      720
tcgccgccgc cttaccaaac ccaccttcc accgcctccc cgccgacgac gacgcgtcgg      780
tgtccgtctc ggtgtcactc tccggcagcg gcgacgcgga cgaacaccgg ggccaccagc      840
acaaacctga gccgcaagaa ccgcgccaac ttgcagggcc gccaccgcac ctgtcagcag      900
ccgccgccgt ctcagcagca cagccgggtg agccatgcgg cgcgcccatg tacgcctgcc      960
accctcagcc acaggaggtg atgtggccgc cgccggctcg tacgccgcac ccgccgccgc     1020
cgccgccgta ctaatccgac cgaattggta cgccattgcc acat                               1064

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<210> 358
<211> 334
<212> PRT
<213> Oryza sativa (japonica cultivar-group)

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<220>
<223> G3408 polypeptide Functionally related and homologous to G1073

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<400> 358

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```

Met Ser Phe Cys Glu Arg Asp Met Asn Lys Glu Ser Met Tyr Gln Glu
1           5           10           15

```

```

Arg Asp Asp Met Ala Gly Ile Arg Phe Ala Thr Pro Pro Leu Pro Gln
20           25           30

```

```

Gln Gln Gln Gln Gln Gln Leu Val Glu Cys Phe Ser Asp Glu Val Asp
35           40           45

```

```

Ser Arg Gly Ser Gly Gly Glu Met Lys Asp Ala Val Gly Ser Gly Ser
50           55           60

```

MBI0058CIP.ST25.txt

Gly Gln Leu Val Val Val Gly Gly Gly Asp Gly Ala Ser Ile Glu Val
65 70 75 80

Ala Lys Lys Arg Arg Gly Arg Pro Pro Gly Ser Lys Asn Lys Pro Lys
85 90 95

Pro Pro Val Val Ile Thr Arg Glu Ala Glu Pro Ala Ala Ala Met Arg
100 105 110

Pro His Val Ile Glu Ile Pro Gly Gly Arg Asp Val Ala Glu Ala Leu
115 120 125

Ala Arg Phe Ser Ser Arg Arg Asn Leu Gly Ile Cys Val Leu Ala Gly
130 135 140

Thr Gly Ala Val Ala Asn Val Ser Leu Arg His Pro Ser Pro Gly Val
145 150 155 160

Pro Gly Ser Ala Pro Ala Ala Ile Val Phe His Gly Arg Tyr Glu Ile
165 170 175

Leu Ser Leu Ser Ala Thr Phe Leu Pro Pro Ala Met Ser Ser Val Ala
180 185 190

Pro Gln Ala Ala Val Ala Ala Ala Gly Leu Ser Ile Ser Leu Ala Gly
195 200 205

Pro His Gly Gln Ile Val Gly Gly Ala Val Ala Gly Pro Leu Tyr Ala
210 215 220

Ala Thr Thr Val Val Val Val Ala Ala Ala Phe Thr Asn Pro Thr Phe
225 230 235 240

His Arg Leu Pro Ala Asp Asp Asp Ala Ser Val Ser Val Ser Val Ser
245 250 255

Leu Ser Gly Ser Gly Asp Ala Asp Glu His Arg Gly His Gln His Lys
260 265 270

Pro Glu Pro Gln Glu Pro Arg Gln Leu Arg Arg Pro Pro Pro His Leu
275 280 285

Ser Ala Ala Ala Ala Val Ser Ala Ala Gln Pro Val Glu Pro Cys Gly
290 295 300

Ala Pro Met Tyr Ala Cys His Pro Gln Pro Gln Glu Val Met Trp Pro
305 310 315 320

Pro Pro Ala Arg Thr Pro His Pro Pro Pro Pro Pro Pro Tyr
325 330

<210> 359
<211> 920
<212> DNA
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3429 Predicted polypeptide sequence is orthologous to G481 and G482

<400> 359
ccagggtcatt gagacttgag agacatggca gggaaacaaaa agcgtggtat agtagtatag 60
tcagtactag gattagtact tgataactag cacaacaaaa agctactatc atttttgcatt 120
tcaaagtggg aattaagaat cggatgatca ttttgattgt tcctcttcat ttgttttgga 180
tgtcagggtgg caggaacatg gatcagggtca agaaggcggc agtgagatcg gatgggggtgg 240
gaggtagtgc gaccaacgcc gagctgccga tggccaacct cgtacgcctg ataaagaagg 300
tgctcccagg gaaagcgaag atcgggggag cagccaaggg tctcacccat gattgcgcgg 360
tggagttcgt cgggttcgtc ggcgacgagg cctccgagaa ggccaaggca gagcaccgcc 420
gcaccgtagc gccggaagac tacttgggct cattcggcga ccttggcttc gatcgctacg 480
tcgaccccat ggatgcctac atccatgggt accgtgaggt tgagagggct ggtgggaata 540
ggaggggtggc gccgcctcct ccggcggcag ctacaccgct gacgcccggg ggaccgacat 600
tcaactgacgc agagctgcag tttctccggt cggatgatccc ctccagaagt gatgatgaat 660
atagcggctc atcaccagcc ataggcggct atggctatgg atatggctat ggaaaaaata 720
tgtgaacaac ttgatgcatg tgtgtgtgta cactgcatgc atgcgtggag ggtcaaacag 780
agtcaagact cttgtggtgg tttcaataag tctctagtga caatataagt tgtgtatcgt 840
tgtttccttt gtaaaaaaaaa aaacgtcatg tatcgttgtg tgcctcatc cggtaatcct 900
ttacgtgggt gggttatggc 920

<210> 360
<211> 193
<212> PRT
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3429 polypeptide Orthologous to G481 and G482

<400> 360

Met Ile Ile Leu Ile Val Pro Leu His Leu Phe Trp Met Ser Gly Gly
1 5 10 15

Arg Asn Met Asp Gln Val Lys Lys Ala Ala Val Arg Ser Asp Gly Val
20 25 30

MBI0058CIP.ST25.txt

Gly Gly Ser Ala Thr Asn Ala Glu Leu Pro Met Ala Asn Leu Val Arg
35 40 45

Leu Ile Lys Lys Val Leu Pro Gly Lys Ala Lys Ile Gly Gly Ala Ala
50 55 60

Lys Gly Leu Thr His Asp Cys Ala Val Glu Phe Val Gly Phe Val Gly
65 70 75 80

Asp Glu Ala Ser Glu Lys Ala Lys Ala Glu His Arg Arg Thr Val Ala
85 90 95

Pro Glu Asp Tyr Leu Gly Ser Phe Gly Asp Leu Gly Phe Asp Arg Tyr
100 105 110

Val Asp Pro Met Asp Ala Tyr Ile His Gly Tyr Arg Glu Phe Glu Arg
115 120 125

Ala Gly Gly Asn Arg Arg Val Ala Pro Pro Pro Pro Ala Ala Ala Thr
130 135 140

Pro Leu Thr Pro Gly Gly Pro Thr Phe Thr Asp Ala Glu Leu Gln Phe
145 150 155 160

Leu Arg Ser Val Ile Pro Ser Arg Ser Asp Asp Glu Tyr Ser Gly Ser
165 170 175

Ser Pro Ala Ile Gly Gly Tyr Gly Tyr Gly Tyr Gly Tyr Gly Lys Asn
180 185 190

Met

<210> 361
<211> 257
<212> DNA
<213> Zea mays

<220>
<223> G3431 Predicted polypeptide sequence is orthologous to G682

<400> 361
ctaattggata gcagcagtgg tagccaggac aagaaattca gagacaatga tcgccttgaa 60
gcaaaagaag ctaatagcac cgcacagcat cttgttgact tcacggaagc agaggaagat 120
cttgtttcca gaatgcacag gcttgtgggg aacaggtggg agattatagc aggaagaatc 180
ccaggaagga cagcagaaga ggtagagatg ttctggtcca aaaaatacca ggaaagatga 240
aaccgaggcc ttagatt 257

<210> 362
 <211> 78
 <212> PRT
 <213> Zea mays

<220>
 <223> G3431 polypeptide Orthologous to G682

<400> 362

Met Asp Ser Ser Ser Gly Ser Gln Asp Lys Lys Phe Arg Asp Asn Asp
 1 5 10 15

Arg Pro Glu Ala Lys Glu Ala Asn Ser Thr Ala Gln His Leu Val Asp
 20 25 30

Phe Thr Glu Ala Glu Glu Asp Leu Val Ser Arg Met His Arg Leu Val
 35 40 45

Gly Asn Arg Trp Glu Ile Ile Ala Gly Arg Ile Pro Gly Arg Thr Ala
 50 55 60

Glu Glu Val Glu Met Phe Trp Ser Lys Lys Tyr Gln Glu Arg
 65 70 75

<210> 363
 <211> 819
 <212> DNA
 <213> Zea mays

<220>
 <223> G3434 Predicted polypeptide sequence is orthologous to G481 and G482

<400> 363

tcgacaaggg ttgcggcgga ggcgcccggg cgctggcgat ggccgacgac ggcgggagcc 60
 acgagggcag cggcgggcgc ggaggcgctc gggagcagga ccggttcctg cccatcgcca 120
 acatcagccg gatcatgaag aaggccgtcc cggccaacgg caagatcgcc aaggacgcta 180
 aggagaccct gcaggagtgc gtctccgagt tcatatcatt cgtgaccagc gaggccagcg 240
 acaaatgcca gaaggagaaa cgaaagacaa tcaacgggga cgatttgctc tgggcgatgg 300
 ccactttagg attcgaggag tacgtcgagc ctctcaagat ttacctacaa aagtacaaag 360
 agatggaggg tgatagcaag ctgtctacaa aggctggcga gggctctgta aagaaggatg 420
 caattagtc ccatggtggc accagtagct caagtaatca gttggttcag catggagtct 480
 acaaccaagg gatgggctat atgcagccac agtaccacaa tggggaaacc taacaaaggg 540
 ctaatacagc agcaatttat gctaggggaag tctctgcatt gcttaccatg tgtattggca 600
 gaaaacagga ggcacttaca aagggtgtta atctctgcga tggctgcctc tcaggtgtaa 660
 attggcttcg gtttagcgct gcttttgtcc gtatatattag gatgatttga ctgttgctac 720

ttttggcaac cttttacatt tacagatatg tattatttcag cataaatata atatagtagt 780
cctaggccta aataatgggtg attaaaaaaaa aaaaaaaaaa 819

<210> 364
<211> 164
<212> PRT
<213> Zea mays

<220>
<223> G3434 polypeptide Orthologous to G481 and G482
<400> 364

Met Ala Asp Asp Gly Gly Ser His Glu Gly Ser Gly Gly Gly Gly Gly
1 5 10 15

Val Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile
20 25 30

Met Lys Lys Ala Val Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys
35 40 45

Glu Thr Leu Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr Ser
50 55 60

Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Ile Asn Gly
65 70 75 80

Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Glu Tyr Val
85 90 95

Glu Pro Leu Lys Ile Tyr Leu Gln Lys Tyr Lys Glu Met Glu Gly Asp
100 105 110

Ser Lys Leu Ser Thr Lys Ala Gly Glu Gly Ser Val Lys Lys Asp Ala
115 120 125

Ile Ser Pro His Gly Gly Thr Ser Ser Ser Ser Asn Gln Leu Val Gln
130 135 140

His Gly Val Tyr Asn Gln Gly Met Gly Tyr Met Gln Pro Gln Tyr His
145 150 155 160

Asn Gly Glu Thr

<210> 365
<211> 735
<212> DNA
<213> Zea mays

<220>

<223> G3435 Predicted polypeptide sequence is orthologous to G481 and G482

<400> 365

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cggcggtggc cttgagctga ggcggcggag cgatgccgga ctcggacaac gactccggcg      60
ggccgagcaa cgccgggggc gagctgtcgt cgccggggga gcaggaccgg ttcctgcca      120
tcgccaacgt gagccggtatc atgaagaagg cgctcccggc caacgccaag atcagcaagg      180
acgccaagga gacggtgcag gagtgcgtgt ccgagttcat ctcttcatc accggcgagg      240
cctccgacaa gtgccagcgc gagaagcgca agaccatcaa cggcgacgac ctgctgtggg      300
ccatgaccac gctcggcttc gaggactacg tcgagccgct caagcactac ctgcacaagt      360
tccgcgagat cgagggcgag agggccgccg cgtccgccgg cgcctcgggc tcgcagcagc      420
agcagcagca gggcgagctg cccagaggcg ccgccaatgc cgccgggtac gccgggtacg      480
gcgcgcctgg ctccggcggc atgatgatga tgatgatggg gcagcccatg tacggcggct      540
cgcagccgca gcaacagccg ccgccgcctc agccgccaca gcagcagcag caacatcaac      600
agcatcacat ggcaatagga ggcagaggag gattcggcca acaaggcggc ggcggcggct      660
cctcgtcgtc gtcagggtt ggccggcaag acagggcggtg agttgcgacg atacgtcaga      720
atcagaatcg ctgat                                          735

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<210> 366

<211> 222

<212> PRT

<213> Zea mays

<220>

<223> G3435 polypeptide Orthologous to G481 and G482

<400> 366

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Met Pro Asp Ser Asp Asn Asp Ser Gly Gly Pro Ser Asn Ala Gly Gly
1          5          10          15

Glu Leu Ser Ser Pro Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn
20          25          30

Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile Ser
35          40          45

Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser
50          55          60

Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys
65          70          75          80

Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe
85          90          95

```

Glu Asp Tyr Val Glu Pro Leu Lys His Tyr Leu His Lys Phe Arg Glu
100 105 110

Ile Glu Gly Glu Arg Ala Ala Ala Ser Ala Gly Ala Ser Gly Ser Gln
115 120 125

Gln Gln Gln Gln Gln Gly Glu Leu Pro Arg Gly Ala Ala Asn Ala Ala
130 135 140

Gly Tyr Ala Gly Tyr Gly Ala Pro Gly Ser Gly Gly Met Met Met Met
145 150 155 160

Met Met Gly Gln Pro Met Tyr Gly Gly Ser Gln Pro Gln Gln Gln Pro
165 170 175

Pro Pro Pro Gln Pro Pro Gln Gln Gln Gln Gln His Gln Gln His His
180 185 190

Met Ala Ile Gly Gly Arg Gly Gly Phe Gly Gln Gln Gly Gly Gly Gly
195 200 205

Gly Ser Ser Ser Ser Ser Gly Leu Gly Arg Gln Asp Arg Ala
210 215 220

<210> 367

<211> 803

<212> DNA

<213> Zea mays

<220>

<223> G3436 Predicted polypeptide sequence is orthologous to G481 and G482

<400> 367

tttgacttga ccggacagtg ctgttcggtg gctcggccgc gatgccggac tccgacaacg 60

agtcggcgcg gccgagcaac gcggagttct cgtcgccgcg ggagcaggac cggttcctgc 120

cgatcgcgaa cgtgagccgg atcatgaaga aggcgctccc ggccaacgcc aagatctcca 180

aggacgccaa ggagacggtg caggagtgcg tgctggagtt catctccttc atcaccggcg 240

aggcctccga caagtgccag cgcgagaagc gcaagaccat caacggcgac gacctactct 300

gggccatgac cacgctcggc ttcgaggact acgtcgagcc gctcaagctc tacctccaca 360

agttccgcga gtcgagggc gagaaggcgg ccacgacgag cgcctcctcc ggcccgcagc 420

cgccgctgca caggagacg acgccgtcgt cgtcaacgca caatggcgcg ggcggggccc 480

tcgggggata cggcatgtac ggcggcgcg gcgggggaag cggtatgatc atgatgatgg 540

gacagcccat gtacggcggc tccccgccgg ccgcgtcgtc cgggtcgtag ccgcaccacc 600

agatggccat gggcggaata ggtggcgctt atggctacgg cggaggctcg tcgtcgtcgc 660

cgtcagggct cggcaggttag gacaggttgt gaccgtcgcc gtccatgctt gcatggccat 720
 ggccatggca tggctcccg cgcgggcttc ttgcttggtg tcggtaatta gcgctgggtg 780
 cctgcgctgg ttaagttcac cat 803

<210> 368
 <211> 212
 <212> PRT
 <213> Zea mays

<220>
 <223> G3436 polypeptide Orthologous to G481 and G482

<400> 368

Met Pro Asp Ser Asp Asn Glu Ser Gly Gly Pro Ser Asn Ala Glu Phe
 1 5 10 15

Ser Ser Pro Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Val Ser
 20 25 30

Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile Ser Lys Asp
 35 40 45

Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile
 50 55 60

Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile
 65 70 75 80

Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe Glu Asp
 85 90 95

Tyr Val Glu Pro Leu Lys Leu Tyr Leu His Lys Phe Arg Glu Leu Glu
 100 105 110

Gly Glu Lys Ala Ala Thr Thr Ser Ala Ser Ser Gly Pro Gln Pro Pro
 115 120 125

Leu His Arg Glu Thr Thr Pro Ser Ser Ser Thr His Asn Gly Ala Gly
 130 135 140

Gly Pro Val Gly Gly Tyr Gly Met Tyr Gly Gly Ala Gly Gly Gly Ser
 145 150 155 160

Gly Met Ile Met Met Met Gly Gln Pro Met Tyr Gly Gly Ser Pro Pro
 165 170 175

Ala Ala Ser Ser Gly Ser Tyr Pro His His Gln Met Ala Met Gly Gly
 180 185 190

Lys Gly Gly Ala Tyr Gly Tyr Gly Gly Gly Ser Ser Ser Ser Pro Ser
195 200 205

Gly Leu Gly Arg
210

<210> 369
<211> 1322
<212> DNA
<213> Zea mays

<220>
<223> G3437 Predicted polypeptide sequence is orthologous to G481 and G482

<400> 369
tattgtctat gaggaagca gatcctctac gctgcaattg ggccactgac atgtgggacc 60
aggtctagat tggaccacaca catcaatgac cgaaatgcag aagaggggtct cgttgccact 120
gtaagctatc tcctagagtt cagagcaggg caagaatctt gcaatgctca catgaacata 180
atataatcgt tgtgttagct atgcgtcggc atcactaccg tcctcccact ggcatctccc 240
gtctactatt ttgggacgaa cagaacagag aactagcta actagcttat tagcttgctc 300
ccctccttcc tttcaagctt taaaaggaga ccatctcttg caccacctct tcatccatcc 360
ggccaagcaa ggggcatgaa gaacaggaag ggctacgggc accagggcca cctgctgagc 420
cccggtgggca gcccgtgtc ggacaacgag tccggcgccg cggcagcggc cggcggcggc 480
gggtgcggga gcagcgtggg gtactgcggc ggcggcgccg gtgagtcgcc ggccaaggag 540
caagaccggt tcctgccgat cgccaacgtg tcgcgcatca tgaagcgctc cctgccggcg 600
aacgccaaga tctccaagga ggccaaggag acggtgcagg agtgcggtgc cgagttcatc 660
agcttcgtca cgggggaggc ctccgacaag tgccagcgcg agaagcgcaa gaccatcaac 720
ggcgacgacc tgctctgggc catgaccacg ctcggtctcg aggcctacgt cgccccgctc 780
aagtcctacc tcaaccgcta ccgcgaggcc gagggcgaga aggccgccgt gctcggcggc 840
ggcgcgcgcc acggcgacgg cgcggcgccg cggacgacgc cggcccactc gccgcgcaat 900
ggcgcgggcg ggcccgtcgg gggatacggc atgtacggcg gcgcggggcg gggaagcggg 960
atgatcatga tgatggggca gcccatgtac ggcggctccc cgccggccgc gtcgtccggg 1020
tcgtaccgc accaccagat ggccatgggc ggaaaagggtg gcgcctatgg ctacggcgga 1080
ggctcgctcg cgtcgccgtc agggctcggc aggtaggcca ggttgtagacc gtcgccgtcc 1140
atgcttgcat ggccatggca tggctcagtc ccgccgccgg cttcttgctt ggtgtcggt 1200
attagcgctg gttaagttaa ccttcggttt tccccctt ttcttttcgt ggtaagtaat 1260
gttggtgctga atggagccag tgatatggtt aagatagctc cataacctct cggtaaaaaa 1320
aa 1322

<210> 370
 <211> 246
 <212> PRT
 <213> Zea mays

<220>
 <223> G3437 polypeptide Orthologous to G481 and G482

<400> 370

Met Lys Asn Arg Lys Gly Tyr Gly His Gln Gly His Leu Leu Ser Pro
 1 5 10 15

Val Gly Ser Pro Leu Ser Asp Asn Glu Ser Gly Ala Ala Ala Ala Ala
 20 25 30

Gly Gly Gly Gly Cys Gly Ser Ser Val Gly Tyr Cys Gly Gly Gly Gly
 35 40 45

Gly Glu Ser Pro Ala Lys Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn
 50 55 60

Val Ser Arg Ile Met Lys Arg Ser Leu Pro Ala Asn Ala Lys Ile Ser
 65 70 75 80

Lys Glu Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser
 85 90 95

Phe Val Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys
 100 105 110

Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe
 115 120 125

Glu Ala Tyr Val Ala Pro Leu Lys Ser Tyr Leu Asn Arg Tyr Arg Glu
 130 135 140

Ala Glu Gly Glu Lys Ala Ala Val Leu Gly Gly Gly Ala Arg His Gly
 145 150 155 160

Asp Gly Ala Ala Arg Arg Thr Thr Pro Ala His Ser Pro Arg Asn Gly
 165 170 175

Ala Gly Gly Pro Val Gly Gly Tyr Gly Met Tyr Gly Gly Ala Gly Gly
 180 185 190

Gly Ser Gly Met Ile Met Met Met Gly Gln Pro Met Tyr Gly Gly Ser
 195 200 205

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Pro Pro Ala Ala Ser Ser Gly Ser Tyr Pro His His Gln Met Ala Met
210 215 220

Gly Gly Lys Gly Gly Ala Tyr Gly Tyr Gly Gly Gly Ser Ser Ser Ser
225 230 235 240

Pro Ser Gly Leu Gly Arg
245

<210> 371
<211> 268
<212> DNA
<213> Zea mays

<220>
<223> G3444 Predicted polypeptide sequence is orthologous to G682

<400> 371
cctaaccctt ctaatggata gcagcagtg tagccaggac aagaaattca gagacaatga 60
tcgccctgaa gcaaaagaag ctaatagcac cgcacagcat cttgttgact tcacggaagc 120
agaggaagat cttgtttcca gaatgcacag gcttgtgggg aacaggtggg agattatagc 180
aggaagaatc ccaggaagga cagcagaaga ggtagagatg ttctggtcca aaaaatacca 240
ggaaagatga aaccgaggcc ttagattt 268

<210> 372
<211> 78
<212> PRT
<213> Zea mays

<220>
<223> G3444 polypeptide Orthologous to G682

<400> 372

Met Asp Ser Ser Ser Gly Ser Gln Asp Lys Lys Phe Arg Asp Asn Asp
1 5 10 15

Arg Pro Glu Ala Lys Glu Ala Asn Ser Thr Ala Gln His Leu Val Asp
20 25 30

Phe Thr Glu Ala Glu Glu Asp Leu Val Ser Arg Met His Arg Leu Val
35 40 45

Gly Asn Arg Trp Glu Ile Ile Ala Gly Arg Ile Pro Gly Arg Thr Ala
50 55 60

Glu Glu Val Glu Met Phe Trp Ser Lys Lys Tyr Gln Glu Arg
65 70 75

<210> 373
<211> 302

<212> DNA

<213> Glycine max

<220>

<223> G3445 Predicted polypeptide sequence is orthologous to G682

<400> 373

```
agaacttggt attgcaatga ctgacataga tcgctcctct gataatgttt cttctgattc      60
tattgagaaa tcaagccaag tttctgatgt tgaattttct gaagctgagg aaatccttat      120
tgccatggtg tataatctgg ttggagaaag gtggtctttg attgctggaa gaattcctgg      180
aagaactgca gaagaaatag agaaatattg gacttcaaga ttttcgacta gccaatgaag      240
tggcagaaat taaacgaagc aagacaattt tgggtgcctg caactcatta tacagtgact      300
ta                                                                    302
```

<210> 374

<211> 73

<212> PRT

<213> Glycine max

<220>

<223> G3445 polypeptide Orthologous to G682

<400> 374

```
Met Thr Asp Ile Asp Arg Ser Ser Asp Asn Val Ser Ser Asp Ser Ile
1           5           10           15

Glu Lys Ser Ser Gln Val Ser Asp Val Glu Phe Ser Glu Ala Glu Glu
          20           25           30

Ile Leu Ile Ala Met Val Tyr Asn Leu Val Gly Glu Arg Trp Ser Leu
          35           40           45

Ile Ala Gly Arg Ile Pro Gly Arg Thr Ala Glu Glu Ile Glu Lys Tyr
          50           55           60

Trp Thr Ser Arg Phe Ser Thr Ser Gln
65           70
```

<210> 375

<211> 257

<212> DNA

<213> Glycine max

<220>

<223> G3446 Predicted polypeptide sequence is orthologous to G682

<400> 375

```
gagaacttgt tatgcaatgg ctgacataga tcgctccttt gataataatg tttctgctgt      60
ttctactgag aaatcaagcc aagtttcaga tggtgaattt tctgaagctg aggaaatcct      120
tattgccatg gtgtataatc tgggtgggga gaggtggtct ttgattgctg gaagaattcc      180
```

tggaagaact gcagaagaga tagagaaata ttggacttca agattttcga ctagccaatg 240
atcgggtggca gaaaacg 257

<210> 376
<211> 74
<212> PRT
<213> Glycine max

<220>
<223> G3446 polypeptide Orthologous to G682

<400> 376

Met Ala Asp Ile Asp Arg Ser Phe Asp Asn Asn Val Ser Ala Val Ser
1 5 10 15

Thr Glu Lys Ser Ser Gln Val Ser Asp Val Glu Phe Ser Glu Ala Glu
20 25 30

Glu Ile Leu Ile Ala Met Val Tyr Asn Leu Val Gly Glu Arg Trp Ser
35 40 45

Leu Ile Ala Gly Arg Ile Pro Gly Arg Thr Ala Glu Glu Ile Glu Lys
50 55 60

Tyr Trp Thr Ser Arg Phe Ser Thr Ser Gln
65 70

<210> 377
<211> 250
<212> DNA
<213> Glycine max

<220>
<223> G3447 Predicted polypeptide sequence is orthologous to G682

<400> 377

gttattgcaa tggctgacat agatcgctcc tttgataata atgtttctgc tgtttctact 60

gagaaatcaa gccaaagtttc agatggttgaa ttttctgaag ctgaggaaat ccttattgcc 120

atgggtgtata atctgggttg ggagaggtgg tctttgattg ctggaagaat tcctggaaga 180

actgcagaag agatagagaa atattggact tcaagatttt cgactagcca atgatcgggtg 240

gcagaaaaacg 250

<210> 378
<211> 74
<212> PRT
<213> Glycine max

<220>
<223> G3447 polypeptide Orthologous to G682

<400> 378

Met Ala Asp Ile Asp Arg Ser Phe Asp Asn Asn Val Ser Ala Val Ser
1 5 10 15

Thr Glu Lys Ser Ser Gln Val Ser Asp Val Glu Phe Ser Glu Ala Glu
20 25 30

Glu Ile Leu Ile Ala Met Val Tyr Asn Leu Val Gly Glu Arg Trp Ser
35 40 45

Leu Ile Ala Gly Arg Ile Pro Gly Arg Thr Ala Glu Glu Ile Glu Lys
50 55 60

Tyr Trp Thr Ser Arg Phe Ser Thr Ser Gln
65 70

<210> 379

<211> 264

<212> DNA

<213> Glycine max

<220>

<223> G3448 Predicted polypeptide sequence is orthologous to G682

<400> 379

attctccacg cctccttgca atggctgact cggatctctc ttcaagtcaa atttctacac	60
attctactga ttcaggaaat cgagggtctt ccaaagttga attttctgaa gatgaggaaa	120
ccctcatcat caggatgtat aaactggtag gggagaggtg gtctataatt gctggaagga	180
ttcctggaag aacagcagag gaaatagaga agtattggac ttcaagattc tcgggctcta	240
gtgaatgaag ctccggagta ctac	264

<210> 380

<211> 75

<212> PRT

<213> Glycine max

<220>

<223> G3448 polypeptide Orthologous to G682

<400> 380

Met Ala Asp Ser Asp Leu Ser Ser Ser Gln Ile Ser Thr His Ser Thr
1 5 10 15

Asp Ser Gly Asn Arg Gly Ser Ser Lys Val Glu Phe Ser Glu Asp Glu
20 25 30

Glu Thr Leu Ile Ile Arg Met Tyr Lys Leu Val Gly Glu Arg Trp Ser
35 40 45

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Ile Ile Ala Gly Arg Ile Pro Gly Arg Thr Ala Glu Glu Ile Glu Lys
50 55 60

Tyr Trp Thr Ser Arg Phe Ser Gly Ser Ser Glu
65 70 75

<210> 381
<211> 268
<212> DNA
<213> Glycine max

<220>
<223> G3449 Predicted polypeptide sequence is orthologous to G682

<400> 381
actcttctag ctccttgcaa tggctgactc ggatcgctct tctagtgaag tttctacaca 60
ttctactgat tcaggggaagc gagggctcttc caaagttgaa ttttctgaag atgaggaaac 120
tcttatcatc aggatgtata aactggtagg ggagaggtgg tctttaattg ctggaaggat 180
tcctggaaga acagcagagg aaatagagaa gtattggact tcaagattct caggttctag 240
tgaatgaggt gccaagagtt ctactacc 268

<210> 382
<211> 75
<212> PRT
<213> Glycine max

<220>
<223> G3449 polypeptide Orthologous to G682

<400> 382

Met Ala Asp Ser Asp Arg Ser Ser Ser Glu Val Ser Thr His Ser Thr
1 5 10 15

Asp Ser Gly Lys Arg Gly Ser Ser Lys Val Glu Phe Ser Glu Asp Glu
20 25 30

Glu Thr Leu Ile Ile Arg Met Tyr Lys Leu Val Gly Glu Arg Trp Ser
35 40 45

Leu Ile Ala Gly Arg Ile Pro Gly Arg Thr Ala Glu Glu Ile Glu Lys
50 55 60

Tyr Trp Thr Ser Arg Phe Ser Gly Ser Ser Glu
65 70 75

<210> 383
<211> 285
<212> DNA
<213> Glycine max

<220>

<223> G3450 Predicted polypeptide sequence is orthologous to G682

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<400> 383
cagctcagaa ggcaaagata gatccatgtc caccaccgca actacaacct ctgaagaagt      60
tagcagcaat gagtggaaag tcatacacat gagcgagcaa gaggaggatc tcattcgcag      120
gatgtacaag ctagtcgggg acaagtggaa tttgatagct ggtcgcattc ccggtcgtaa      180
agcagaagaa atagagagat tctggattat gagacacggc gatgcttttt ctgttaaaag      240
aaacggaagt aaaaccaag actcgtgatt ttctctggtc atgta                        285
```

```
<210> 384
<211> 80
<212> PRT
<213> Glycine max
```

<220>

<223> G3450 polypeptide Orthologous to G682

<400> 384

```
Met Ser Thr Thr Ala Thr Thr Thr Ser Glu Glu Val Ser Ser Asn Glu
1          5          10          15
```

```
Trp Lys Val Ile His Met Ser Glu Gln Glu Glu Asp Leu Ile Arg Arg
          20          25          30
```

```
Met Tyr Lys Leu Val Gly Asp Lys Trp Asn Leu Ile Ala Gly Arg Ile
          35          40          45
```

```
Pro Gly Arg Lys Ala Glu Glu Ile Glu Arg Phe Trp Ile Met Arg His
          50          55          60
```

```
Gly Asp Ala Phe Ser Val Lys Arg Asn Gly Ser Lys Thr Gln Asp Ser
65          70          75          80
```

```
<210> 385
<211> 869
<212> DNA
<213> Glycine max
```

<220>

<223> G3456 Predicted polypeptide sequence is orthologous to G1073

```
<400> 385
tcgacaactt caacttttgt tatggccaac cggtggtgga cggggtcggg ggggtctagag      60
aactctggcc actcgatgaa aaaaccggat ctgggggtttt ccatgaacga gagtacggtg      120
acggggaacc atataggaga agaagatgag gacagagaaa acagcgacga gccaagagag      180
ggagctattg acgtcgccac cacgcgccgc cctaggggac gtccaccggg ctccagaaac      240
aagccgaaac cgccgatatt cgtcacccga gacagcccta acgcgctgcg gagccacgtc      300
atggagattg ccgtcggagc cgacatcgcc gactgcgtgg cgcagttcgc tcggaggcgc      360
```

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```

cagcgcggggg tttccattct cagcggcagc gggaccgtcg tcaacgtcaa tctccggcaa 420
cccacggcac ccggcgccgt catggcgctc cacggccgct tcgacatcct ctccctcacc 480
ggctcctttc tccctgggccc gtccctccc ggcgccaccg ggctcacaat ctacctcgcc 540
ggaggccagg ggcagatcgt cggcggcgga gtggtgggccc cgctcgtggc ggcgggcccc 600
gtattggttaa tggcggctac tttttccaat gctacgtatg aaagattgcc tttagaggat 660
gatgatcagg aacaacacgg cggcggaggc ggaggagggt cgccgcagga aaaaaccggg 720
ggccccggcg aggcgtcgtc gtcgatttcg gtttataaca ataatgttcc tccgagttta 780
gggtcttccga atgggcaaca tctgaaccat gaagcttatt cttctccttg gggtcattct 840
cctcatgcca gacctccttt ctaattagc 869

```

```

<210> 386
<211> 262
<212> PRT
<213> Glycine max

```

```

<220>
<223> G3456 polypeptide Orthologous to G1073

```

```

<400> 386

```

```

Met Lys Lys Pro Asp Leu Gly Phe Ser Met Asn Glu Ser Thr Val Thr
1          5          10          15

```

```

Gly Asn His Ile Gly Glu Glu Asp Glu Asp Arg Glu Asn Ser Asp Glu
          20          25          30

```

```

Pro Arg Glu Gly Ala Ile Asp Val Ala Thr Thr Arg Arg Pro Arg Gly
          35          40          45

```

```

Arg Pro Pro Gly Ser Arg Asn Lys Pro Lys Pro Pro Ile Phe Val Thr
          50          55          60

```

```

Arg Asp Ser Pro Asn Ala Leu Arg Ser His Val Met Glu Ile Ala Val
          65          70          75          80

```

```

Gly Ala Asp Ile Ala Asp Cys Val Ala Gln Phe Ala Arg Arg Arg Gln
          85          90          95

```

```

Arg Gly Val Ser Ile Leu Ser Gly Ser Gly Thr Val Val Asn Val Asn
          100          105          110

```

```

Leu Arg Gln Pro Thr Ala Pro Gly Ala Val Met Ala Leu His Gly Arg
          115          120          125

```

```

Phe Asp Ile Leu Ser Leu Thr Gly Ser Phe Leu Pro Gly Pro Ser Pro
          130          135          140

```

Pro Gly Ala Thr Gly Leu Thr Ile Tyr Leu Ala Gly Gly Gln Gly Gln
145 150 155 160

Ile Val Gly Gly Gly Val Val Gly Pro Leu Val Ala Ala Gly Pro Val
165 170 175

Leu Val Met Ala Ala Thr Phe Ser Asn Ala Thr Tyr Glu Arg Leu Pro
180 185 190

Leu Glu Asp Asp Asp Gln Glu Gln His Gly Gly Gly Gly Gly Gly Gly
195 200 205

Ser Pro Gln Glu Lys Thr Gly Gly Pro Gly Glu Ala Ser Ser Ser Ile
210 215 220

Ser Val Tyr Asn Asn Asn Val Pro Pro Ser Leu Gly Leu Pro Asn Gly
225 230 235 240

Gln His Leu Asn His Glu Ala Tyr Ser Ser Pro Trp Gly His Ser Pro
245 250 255

His Ala Arg Pro Pro Phe ,
260

<210> 387
<211> 1153
<212> DNA
<213> Glycine max

<220>
<223> G3458 Functionally related and homologous to G1073

<400> 387
tcgcccacgc gtccgtacgg ctgcgagaag acgacagaag gggccacttt atttgtctct 60
ctctttccct tccaacctca tcccattccg ttttctctgc agtactcaat tgatcccttt 120
gtttttctat tcgttctgag agctttgtgt gtatggccgg catagacttg ggttcagcat 180
cacattttgt tcatcatcgc cttgaacgcc ctgacctga agacgatgag aaccaacaag 240
accaagacaa caaccttaac aatcacgaag ggcttgacct agttacacca aattcaggtc 300
ctggtgatgt tggtggtcgc aggccaagag gaagacctcc aggttcaaag aacaagccaa 360
aaccaccagt tatcatcaca agagagagtg caaacacct tagggctcac atccttgaag 420
ttagtagtgg ttgtgacgtc tttgaatcgg tcgctacct tgcaaggaag cgacaaagag 480
ggatctgtgt cctcagtggg agtggcaccg tgaccaacgt gacattgagg cagccggccg 540
cggctgggtgc cgtcgtcacg ctgcacggaa gggttgagat cctctctttg tcaggatcat 600
tcctcccacc tccagctcca ccaggtgcta caagtttgac tgtgttcctt ggtggaggac 660
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```

agggtcaagt ggtgggagga aatgttggtg gtcttttggg ggcttctggg cctggtattg      720
ttattgcttc atcttttact aatgtagcat atgagagggt gccttttgat gaagatgaat      780
ctatgcagat gcaacaaggg caatcatcag ctggtgatgg tagcggtgac catggtggtg      840
gagttagtaa taactctttt ccggatccgt cttccgggct tccattcttc aatttgccac      900
taaacatgcc tcagttacct gttgatgggt gggctggcaa ctctggtgga aggcaatctt      960
actgatccag agtctttggg ggcacaaagg tgagaagttg aattgatctc atatatattg     1020
gtcttctcta atctttcttc tgaatattgc ttgtgaagaa gtactgattt ttctattgaa     1080
gaaatcgttt gtttggctag gtttggtgta aggacgatca gtttctagga acaactgtaa     1140
aacgttttct ctt                                                         1153

```

<210> 388

<211> 270

<212> PRT

<213> Glycine max

<220>

<223> G3458 polypeptide Functionally related and homologous to G1073

<400> 388

```

Met Ala Gly Ile Asp Leu Gly Ser Ala Ser His Phe Val His His Arg
1           5           10           15

```

```

Leu Glu Arg Pro Asp Leu Glu Asp Asp Glu Asn Gln Gln Asp Gln Asp
                20           25           30

```

```

Asn Asn Leu Asn Asn His Glu Gly Leu Asp Leu Val Thr Pro Asn Ser
35           40           45

```

```

Gly Pro Gly Asp Val Val Gly Arg Arg Pro Arg Gly Arg Pro Pro Gly
50           55           60

```

```

Ser Lys Asn Lys Pro Lys Pro Pro Val Ile Ile Thr Arg Glu Ser Ala
65           70           75           80

```

```

Asn Thr Leu Arg Ala His Ile Leu Glu Val Ser Ser Gly Cys Asp Val
                85           90           95

```

```

Phe Glu Ser Val Ala Thr Tyr Ala Arg Lys Arg Gln Arg Gly Ile Cys
                100          105          110

```

```

Val Leu Ser Gly Ser Gly Thr Val Thr Asn Val Thr Leu Arg Gln Pro
115           120           125

```

```

Ala Ala Ala Gly Ala Val Val Thr Leu His Gly Arg Phe Glu Ile Leu
130           135           140

```


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Ser Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala Pro Pro Gly Ala Thr
145 150 155 160

Ser Leu Thr Val Phe Leu Gly Gly Gly Gln Gly Gln Val Val Gly Gly
165 170 175

Asn Val Val Gly Pro Leu Val Ala Ser Gly Pro Val Ile Val Ile Ala
180 185 190

Ser Ser Phe Thr Asn Val Ala Tyr Glu Arg Leu Pro Leu Asp Glu Asp
195 200 205

Glu Ser Met Gln Met Gln Gln Gly Gln Ser Ser Ala Gly Asp Gly Ser
210 215 220

Gly Asp His Gly Gly Gly Val Ser Asn Asn Ser Phe Pro Asp Pro Ser
225 230 235 240

Ser Gly Leu Pro Phe Phe Asn Leu Pro Leu Asn Met Pro Gln Leu Pro
245 250 255

Val Asp Gly Trp Ala Gly Asn Ser Gly Gly Arg Gln Ser Tyr
260 265 270

<210> 389
<211> 1596
<212> DNA
<213> Glycine max

<220>
<223> G3459 Functionally related and homologous to G1073

<400> 389
ctgtcgcgtg ggaaacaaat ggctgcattg tgagttcttt gtcccccttca acctcatttc 60
aattctctct ctccccatt cttacttcac ccgcgcccc tcccccgccc gctcccgctcc 120
cttttctttt tctgcactcc atctttcttt ccaaaaccca cccttttcta ttctcttcc 180
tcttctctct tttcccttct ttttatttcc ttacactcac aacatttccc ttaaaataaa 240
cataaaca aaa ccagcactgt tcttgacccc caaaaaaaaa aaatctctac tatttattaa 300
ctatattaat tcctccataa tataatcatt tgttttcctt gttttctgtt ttctcttata 360
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tttaggaagc gcctcacgct ttgttcaaaa ctttcacaga ccagacttgc acttgcaaca 540
aaatttccag cagcaccagg accagcagca ccagcgtgat ttggaggagc agaaaactcc 600
tccgaatcac agaattgggg cgccgttcga cgatgatagc gatgatagaa gcccgggcct 660

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ggagctcact tcaggtcctg gcgacatcgt cggacggcgc ccgcgtggca ggcctcctgg      720
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ggcgcacatc ctcgaggtcg gaagcggctc cgacgtcttc gactgtgtca ccgcgtatgc      840
ccggcggcgc cagcgtggga tctgcgtcct cagtggcagc ggcaccgtca ccaatgtcag      900
tctccggcag cctgcagctg ccggtgccgt cgtcacgctg cacggcaggt tcgagattct      960
ctccctctct ggctcgttcc tcccgcgcgc ggctccgccc ggagccacca gcctcacaat    1020
ctacctggcc ggcgggcagg ggcaggttgt cggaggaaac gtcacgagag aattaaccgc    1080
agcagggcca gtaatcgtca tcgcagcgtc gttcaccaac gtggcttacg agaggttacc    1140
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gttggttaatg gatataatat gacatgataa ttattatgta gtctgatttt catctccttg    1560
gaattttata tacttatttc ccctgttaaa aaaaaa                                1596

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<210> 390

<211> 295

<212> PRT

<213> Glycine max

<220>

<223> G3459 polypeptide Functionally related and homologous to G1073

<400> 390

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Met Ala Gly Leu Asp Leu Gly Ser Ala Ser Arg Phe Val Gln Asn Leu
1           5           10          15

```

```

His Arg Pro Asp Leu His Leu Gln Gln Asn Phe Gln Gln His Gln Asp
          20          25          30

```

```

Gln Gln His Gln Arg Asp Leu Glu Glu Gln Lys Thr Pro Pro Asn His
          35          40          45

```

```

Arg Met Gly Ala Pro Phe Asp Asp Asp Ser Asp Asp Arg Ser Pro Gly
          50          55          60

```

```

Leu Glu Leu Thr Ser Gly Pro Gly Asp Ile Val Gly Arg Arg Pro Arg
65          70          75          80

```

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Gly Arg Pro Pro Gly Ser Lys Asn Lys Pro Lys Pro Pro Val Ile Ile
85 90 95

Thr Arg Glu Ser Ala Asn Thr Leu Arg Ala His Ile Leu Glu Val Gly
100 105 110

Ser Gly Ser Asp Val Phe Asp Cys Val Thr Ala Tyr Ala Arg Arg Arg
115 120 125

Gln Arg Gly Ile Cys Val Leu Ser Gly Ser Gly Thr Val Thr Asn Val
130 135 140

Ser Leu Arg Gln Pro Ala Ala Ala Gly Ala Val Val Thr Leu His Gly
145 150 155 160

Arg Phe Glu Ile Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala
165 170 175

Pro Pro Gly Ala Thr Ser Leu Thr Ile Tyr Leu Ala Gly Gly Gln Gly
180 185 190

Gln Val Val Gly Gly Asn Val Ile Gly Glu Leu Thr Ala Ala Gly Pro
195 200 205

Val Ile Val Ile Ala Ala Ser Phe Thr Asn Val Ala Tyr Glu Arg Leu
210 215 220

Pro Leu Glu Glu Asp Glu Gln Gln Gln Gln Gln Gln Gln Leu Gln Ile
225 230 235 240

Gln Pro Pro Ala Thr Thr Ser Ser Gln Gly Asn Asn Asn Asn Asn Asn
245 250 255

Pro Phe Pro Asp Pro Ser Ser Gly Leu Pro Phe Phe Asn Leu Pro Leu
260 265 270

Asn Met Gln Asn Val Gln Leu Pro Val Glu Gly Trp Ala Val Asn Pro
275 280 285

Ala Ser Arg Pro Gln Pro Phe
290 295

<210> 391
<211> 1443
<212> DNA
<213> Glycine max

<220>
<223> G3460 PFunctionally related and homologous to G1073

MBI0058CIP.ST25.txt

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aaaaaattat ctactattta ttaactatat ttctccatat tataatcatt tgtattcctt      180
gttttctatg cttctcttat aatatataac cttcgtttta tttatttttt ttgttttgca      240
ccttgtggat tgtgagctat atctatttat atatatcatt ctctttcttt ttttttgat      300
gtttctatgg ctggtttgga tttaggaagc gcgtcacgct ttgttcagaa tcttcactta      360
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caagagactc ctccgaacct gggaacagcg ctggcgccgt tcgacaacga tgatgacaaa      480
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agaccttccg ggtccaagaa caagccgaag ccaccggtga taatcacccg ggagagcgcc      600
aacacgctga gggcgcacat tctcgaggta ggaagcggct ccgacgtctt cgactgtgtc      660
accgcttatg cgcgggcgcg ccagcgcggg atctgcgtcc tcagcggcag tggcacgctc      720
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cttcccttct tcaacttacc actcaatatg cagaatgttc agttaccacc tttttgaggg     1140
ttcatgaatc tgataatatg agactgatga agatcatggt gatggaggat ttatcaccaa     1200
agggtttata ttattataag gtcagcaaat attcatggac tagaacatat atataaacta     1260
tatgttcttc ttcttcttgt tagtatgttt tttttttctt ctgttggtta tgggtatcgt     1320
tatgatagga catgattatt attattatgt agcgagtttc agtctgactc tcatgtcttt     1380
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att                                                                                   1443

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<210> 392
<211> 276
<212> PRT
<213> Glycine max

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<220>
<223> G3460 polypeptide Functionally related and homologous to G1073

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<400> 392

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Met Ala Gly Leu Asp Leu Gly Ser Ala Ser Arg Phe Val Gln Asn Leu
1           5           10          15

```

His Leu Pro Asp Leu His Leu Gln Gln Asn Tyr Gln Gln Pro Arg His
20 25 30

Lys Arg Asp Ser Glu Glu Gln Glu Thr Pro Pro Asn Pro Gly Thr Ala
35 40 45

Leu Ala Pro Phe Asp Asn Asp Asp Asp Lys Ser Gln Gly Leu Glu Leu
50 55 60

Ala Ser Gly Pro Gly Asp Ile Val Gly Arg Arg Pro Arg Gly Arg Pro
65 70 75 80

Ser Gly Ser Lys Asn Lys Pro Lys Pro Pro Val Ile Ile Thr Arg Glu
85 90 95

Ser Ala Asn Thr Leu Arg Ala His Ile Leu Glu Val Gly Ser Gly Ser
100 105 110

Asp Val Phe Asp Cys Val Thr Ala Tyr Ala Arg Arg Arg Gln Arg Gly
115 120 125

Ile Cys Val Leu Ser Gly Ser Gly Thr Val Thr Asn Val Ser Leu Arg
130 135 140

Gln Pro Ala Ala Ala Gly Ala Val Val Arg Leu His Gly Arg Phe Glu
145 150 155 160

Ile Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala Pro Pro Gly
165 170 175

Ala Thr Ser Leu Thr Ile Tyr Leu Ala Gly Gly Gln Gly Gln Val Val
180 185 190

Gly Gly Asn Val Val Gly Glu Leu Thr Ala Ala Gly Pro Val Ile Val
195 200 205

Ile Ala Ala Ser Phe Thr Asn Val Ala Tyr Glu Arg Leu Pro Leu Glu
210 215 220

Glu Asp Glu Gln Gln His Gln Gln Leu Gln Ile Gln Ser Pro Ala Ala
225 230 235 240

Thr Ser Ser Gln Gly Asn Asn Asn Asn Asn Pro Phe Pro Asp Pro Ser
245 250 255

Ser Gly Leu Pro Phe Phe Asn Leu Pro Leu Asn Met Gln Asn Val Gln
260 265 270

Leu Pro Pro Phe
275

<210> 393
<211> 1611
<212> DNA
<213> Glycine max

<220>
<223> G3462 Predicted polypeptide sequence is orthologous to G1073

<400> 393
ccacgcgtcc gcactctaag gtacttcccc actgttccca ttttatgccc gtactagtct 60
gacccttttta gtggcataga ttgaggtaca attacaaaag catattaccc gtatcgtatc 120
ctttctgcta caaccacccc gaaacacact gcgttttttt tgtgtcaaac ttcaaccggg 180
gctttctttac ttctcttctc ttcaactttt tagtgttttt tttttttttt tctcgtgtcg 240
ggtccttgag cttctatttg tttatatttt tccggcagcg agttgagtta attttcgtgt 300
catagtctca attaggtgga tgtgacttgt gtgggttaggg tttacatgca aaaacgcatg 360
tgcttcgggt ctaattcatc ctgaaacaag gttttgggac agagatctga atatttcaag 420
ctatctattt tgtttctcta tctagaaggt tttgagaaat caaagatggc gaatagatgg 480
tgggctggga atgtgggaat gataagagag caagagttga tggaaaacag caacaacaac 540
aacaacaaca acaacgctac tactactaca ccgacgacga ggagcaacag caacactaac 600
gcgaacacca acaccaacac gaccgaggaa gaggtgagca gggataacgg agaggaccag 660
aaccaaaacc tcggcagcca cgaagggtcg gagcccgga gcagcggtcg gagggcacgt 720
ggcaggccag cggggtccaa gaacaagccc aagccgccc tagtcataat ttttttaagc 780
cccaacgcgc tccgaagcca cgtcctggaa atcgccctcg gccgcgatgt cgccgagagc 840
atcgccgcct tcgccaaccg ccgccaccgt ggcgtgtcgg tcctcagcgg gagtggcatt 900
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cagcagcagc agcaacagca gcagcagcag cagcagcaac aacaatctca aggtttgggg 1260
gaacaggttt caatgcctat gtataatttg cctcctaatt tgctacacaa tggtcagaac 1320
atgcctcatg atgtgttctg gggagctcca cctcgccctc ctccctcctt ctgatcacc 1380
ttgccaatat gatcatgtct ttaatctctc actgacttgc gaattaagta ctatgttaat 1440
taatttctca cgggtttttt tgcaagcata gctagctagc tagcaagggt agttattagg 1500

atgggtttgt taatttgcgc ttcttagaga ctgcagtgcaa gtagatgatg ttcttatctt 1560
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<210> 394
 <211> 302
 <212> PRT
 <213> Glycine max

<220>
 <223> G3462 polypeptide Orthologous to G1073

<400> 394

Met Ala Asn Arg Trp Trp Ala Gly Asn Val Gly Met Ile Arg Glu Gln
 1 5 10 15

Glu Leu Met Glu Asn Ser Asn Asn Asn Asn Asn Asn Asn Ala Thr
 20 25 30

Thr Thr Thr Pro Thr Thr Arg Ser Asn Ser Asn Thr Asn Ala Asn Thr
 35 40 45

Asn Thr Asn Thr Thr Glu Glu Glu Val Ser Arg Asp Asn Gly Glu Asp
 50 55 60

Gln Asn Gln Asn Leu Gly Ser His Glu Gly Ser Glu Pro Gly Ser Ser
 65 70 75 80

Gly Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys Asn Lys Pro Lys
 85 90 95

Pro Pro Ile Val Ile Ile Phe Leu Ser Pro Asn Ala Leu Arg Ser His
 100 105 110

Val Leu Glu Ile Ala Ser Gly Arg Asp Val Ala Glu Ser Ile Ala Ala
 115 120 125

Phe Ala Asn Arg Arg His Arg Gly Val Ser Val Leu Ser Gly Ser Gly
 130 135 140

Ile Val Ala Asn Val Thr Leu Arg Gln Pro Ala Ala Pro Ala Gly Val
 145 150 155 160

Ile Thr Leu His Gly Arg Phe Glu Ile Leu Ser Leu Ser Gly Ala Phe
 165 170 175

Leu Pro Ser Pro Ser Pro Ser Gly Ala Thr Gly Leu Thr Val Tyr Leu
 180 185 190

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Ala Gly Gly Gln Gly Gln Val Val Gly Gly Asn Val Ala Gly Ser Leu
195 200 205

Val Ala Ser Gly Pro Val Met Val Ile Ala Ala Thr Phe Ala Asn Ala
210 215 220

Thr Tyr Glu Arg Leu Pro Leu Glu Asp Asp Gln Gly Glu Glu Glu Met
225 230 235 240

Gln Val Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
245 250 255

Gln Gln Gln Gln Ser Gln Gly Leu Gly Glu Gln Val Ser Met Pro Met
260 265 270

Tyr Asn Leu Pro Pro Asn Leu Leu His Asn Gly Gln Asn Met Pro His
275 280 285

Asp Val Phe Trp Gly Ala Pro Pro Arg Pro Pro Pro Ser Phe
290 295 300

<210> 395
<211> 555
<212> DNA
<213> Glycine max

<220>
<223> G3470 Predicted polypeptide sequence is orthologous to G481 and G482

<400> 395
tcaccggggtt tgtgagatgt cggatgcacc ggcgagtccg agtcacgaga gtggtggcga 60
gcagagccct cgcggtctgt tgtccggcgc ggctagagag caggaccggt accttcccat 120
tgccaacatc agccgcatca tgaagaaggc tctgcctccc aatggcaaga ttgcgaagga 180
tgcaaaagac acaatgcaag aatgcgtttc tgaattcatc agcttcatta ccagcgaggc 240
gagtgaagaa tgccagaagg agaagagaaa gacaatcaat ggagacgatt tactatgggc 300
catggcaact ttagggtttg aagactacat tgagccgctt aaggtgtacc tggctaggta 360
cagagaggcg gaggggtgaca ctaaaggatc tgctagaagt ggtgatggat ctgctagacc 420
agatcaagtt ggccttgag gtcaaaatgc tcagcttggt catcagggtt cgctgaacta 480
tattggtttg caggtgcaac cacaacatct ggttatgcct tcaatgcaag gccatgaata 540
gtttgatgac ttcta 555

<210> 396
<211> 174
<212> PRT
<213> Glycine max

<220>

<223> G3470 polypeptide Orthologous to G481 and G482

<400> 396

Met Ser Asp Ala Pro Ala Ser Pro Ser His Glu Ser Gly Gly Glu Gln
1 5 10 15

Ser Pro Arg Gly Ser Leu Ser Gly Ala Ala Arg Glu Gln Asp Arg Tyr
20 25 30

Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala Leu Pro Pro
35 40 45

Asn Gly Lys Ile Ala Lys Asp Ala Lys Asp Thr Met Gln Glu Cys Val
50 55 60

Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Glu Lys Cys Gln
65 70 75 80

Lys Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met
85 90 95

Ala Thr Leu Gly Phe Glu Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu
100 105 110

Ala Arg Tyr Arg Glu Ala Glu Gly Asp Thr Lys Gly Ser Ala Arg Ser
115 120 125

Gly Asp Gly Ser Ala Arg Pro Asp Gln Val Gly Leu Ala Gly Gln Asn
130 135 140

Ala Gln Leu Val His Gln Gly Ser Leu Asn Tyr Ile Gly Leu Gln Val
145 150 155 160

Gln Pro Gln His Leu Val Met Pro Ser Met Gln Gly His Glu
165 170

<210> 397

<211> 556

<212> DNA

<213> Glycine max

<220>

<223> G3471 Predicted polypeptide sequence is orthologous to G481 and G482

<400> 397

gtaggggtttg tgagatgtcg gatgcgccac cgagcccgac tcatgagagt gggggcgagc 60

agagcccgcg cggttcgtcg tccggcgcgga gggagcagga ccggtacctc ccgattgcca 120

acatcagccg cattatgaag aaggctctgc ctcccaacgg caagattgca aaggatgcca 180

aagacaccat gcaggaatgc gtttctgagt tcatcagctt cattaccagc gaggcgagtg 240

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agaaatgcca gaaggagaag agaaagacaa tcaatggaga cgatttgcta tgggccatgg      300
ccactttagg atttgaagac tacatagagc cgcttaaggt gtacctggct aggtacagag      360
aggcggaggg tgacactaaa ggatctgcta gaagtgggtga tggatctgct acaccagatc      420
aagttggcct tgcaggtcaa aattctcagc ttgttcatca gggttcgctg aactatattg      480
gtttgcaggt gcaaccacaa catctgggta tgccttcaat gcaaagccat gaatagttta      540
gatgcttcta cgcac                                     556

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```

<210> 398
<211> 173
<212> PRT
<213> Glycine max

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```

<220>
<223> G3471 polypeptide Orthologous to G481 and G482
<400> 398

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```

Met Ser Asp Ala Pro Pro Ser Pro Thr His Glu Ser Gly Gly Glu Gln
1          5          10          15

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```

Ser Pro Arg Gly Ser Ser Ser Gly Ala Arg Glu Gln Asp Arg Tyr Leu
          20          25          30

```

```

Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala Leu Pro Pro Asn
          35          40          45

```

```

Gly Lys Ile Ala Lys Asp Ala Lys Asp Thr Met Gln Glu Cys Val Ser
          50          55          60

```

```

Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Glu Lys Cys Gln Lys
65          70          75          80

```

```

Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Ala
          85          90          95

```

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Thr Leu Gly Phe Glu Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu Ala
          100          105          110

```

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Arg Tyr Arg Glu Ala Glu Gly Asp Thr Lys Gly Ser Ala Arg Ser Gly
          115          120          125

```

```

Asp Gly Ser Ala Thr Pro Asp Gln Val Gly Leu Ala Gly Gln Asn Ser
          130          135          140

```

```

Gln Leu Val His Gln Gly Ser Leu Asn Tyr Ile Gly Leu Gln Val Gln
145          150          155          160

```

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Pro Gln His Leu Val Met Pro Ser Met Gln Ser His Glu
165 170

<210> 399
<211> 547
<212> DNA
<213> Glycine max

<220>
<223> G3472 Predicted polypeptide sequence is orthologous to G481 and G482

<400> 399
taaggctagc tagctagcca tggctgagtc ggacaacgag tccggaggtc acacggggaa 60
cgcaagcgga agcaacgaat tctccggttg caggagagcaa gacagggttc ttccgatagc 120
gaacgtgagc aggatcatga agaaggcggt gccggcggaac gcgaagatct cgaaggaggc 180
gaaggagacg gtgcaggagt gcgtgtcgga gttcatcagc ttcataacag gagaagcgtc 240
cgataagtgc cagaaggaga agaggaagac gatcaacggc gatgatctgc tgtggggccat 300
gaccacgctg ggattcgagg agtacgtgga gcctctcaag gtttatctgc ataagtatag 360
ggagctggaa ggggagaaaa ctgctatgat ggggaaggcca catgagaggg atgagggtta 420
tggtcatgca actcctatga tgatcatgat ggggcatcaa cagcagcagc atcagggaca 480
cgtgtatgga tctggaacta ctactggatc agcatcttct gcaagaacta gataacaggt 540
ttatgca 547

<210> 400
<211> 171
<212> PRT
<213> Glycine max

<220>
<223> G3472 polypeptide Orthologous to G481 and G482

<400> 400

Met Ala Glu Ser Asp Asn Glu Ser Gly Gly His Thr Gly Asn Ala Ser
1 5 10 15

Gly Ser Asn Glu Phe Ser Gly Cys Arg Glu Gln Asp Arg Phe Leu Pro
20 25 30

Ile Ala Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala
35 40 45

Lys Ile Ser Lys Glu Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu
50 55 60

Phe Ile Ser Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Lys Glu
65 70 75 80

MBI0058CIP.ST25.txt

Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr
85 90 95

Leu Gly Phe Glu Glu Tyr Val Glu Pro Leu Lys Val Tyr Leu His Lys
100 105 110

Tyr Arg Glu Leu Glu Gly Glu Lys Thr Ala Met Met Gly Arg Pro His
115 120 125

Glu Arg Asp Glu Gly Tyr Gly His Ala Thr Pro Met Met Ile Met Met
130 135 140

Gly His Gln Gln Gln Gln His Gln Gly His Val Tyr Gly Ser Gly Thr
145 150 155 160

Thr Thr Gly Ser Ala Ser Ser Ala Arg Thr Arg
165 170

<210> 401

<211> 1818

<212> DNA

<213> Glycine max

<220>

<223> G3473 Predicted polypeptide sequence is orthologous to G481 and G482

<400> 401

tttttaaata ataaaatggt tctttggaaa tttcttaaaa agtatgaaca taaatttaaa	60
ttattatttt atattaaatg cacttatggt aatttatgtg tcttgcatac acatttaatg	120
ttatccttct ttatatctat attaaactat atatataaag aaaagatttt gaaatttgaa	180
taagataaga gtgtccaggt cagaggcgag cacgtgccag ataccaaagc aacgggtccag	240
atcatggagc actcaccaaa tccaagggct ccaattcgtc cgtggacact cacacttatc	300
gactaacaac ggtccacaaa tcgccacgtg tcctcaagat aaagcggtat taacccttct	360
gatccaacgg atcctgctca ttatctccca aacaaacccc tccgttccgt ttcaccttct	420
cccttccgc cggagccgcc gtcaccggtc gctggccacc gtatccgacc ctccaatac	480
accctttccg agtcccacac aaaattgcac gattctgtga tttcaatttt caggtctcga	540
ggatttcgtt tcagaagcgc ttccatttga cgcagaacca ccgactcaaa ccgattcgcg	600
ccgagttcgt gactcgaatt ttcaacttct cattcatatt ccaaactgaa ttgaaactc	660
cgaagaaaaa ttcaccgaac actgaatctc agtttccaag gagcttcttc tacgaagagc	720
gcttcaattc cagcagaac caccaagtca agccgggttcg tgactcggat tctcaattcc	780
tcgttcattc ccgaacgaat tttaaattcc gaagaaaacc gcaccgaaca ctgaatttca	840
gattctgaac aagtttcttc cgcgaaacag cacagcactt caatttcacg tggaacagag	900

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 attttccctg cactgactta gtgattcggt tcatctttct cagcgcgtct tcgatttttc 1080
 cgttagtcga tggcgggactc cgacaacgac tccggcggcg cgcacaacgg cggcaagggg 1140
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 atgaagaagg cgctgccggc gaacgcgaag atctcgaagg acgcgaagga gacggtgcag 1260
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 atctcatctg ttttaagctta ttaaggggtg tcttttttga tgggtgatttt gtttgatttt 1680
 agaaacaccc cagctccagc ttgtaattgt tgcttgaaac ttcgttggtg agagaatata 1740
 gccattattg tggatggtga tgtgacatgc acagaatttt tgtattcttc tttcttccaa 1800
 tggatttatc tcggggccc 1818

<210> 402

<211> 170

<212> PRT

<213> Glycine max

<220>

<223> G3473 polypeptide Orthologous to G481 and G482

<400> 402

Met Ala Asp Ser Asp Asn Asp Ser Gly Gly Ala His Asn Gly Gly Lys
 1 5 10 15

Gly Ser Glu Met Ser Pro Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala
 20 25 30

Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile
 35 40 45

Ser Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile
 50 55 60

Ser Phe His Ser Pro Gly Gly Leu Ala Gly Glu Cys Gln Lys Glu Lys
 65 70 75 80

Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu

Gly Phe Glu Glu Tyr Val Glu Pro Leu Lys Val Tyr Leu His Lys Tyr
100 105 110

Arg Glu Leu Glu Gly Glu Lys Thr Ala Met Met Gly Arg Pro His Glu
115 120 125

Arg Asp Glu Gly Tyr Gly His Ala Thr Pro Met Met Ile Met Met Gly
130 135 140

His Gln Gln Gln Gln His Gln Gly His Val Tyr Gly Ser Gly Thr Thr
145 150 155 160

Thr Gly Ser Ala Ser Ser Ala Arg Thr Arg
165 170

<210> 403
<211> 553
<212> DNA
<213> Glycine max

<220>
<223> G3474 Predicted polypeptide sequence is orthologous to G481 and G482

<400> 403
gatatccatg gctgagtcg acaacgagtc aggaggtcac acggggaacg cgagcgggag 60
caacgagttg tccggttgca gggagcaaga caggttcctc ccaatagcaa acgtgagcag 120
gatcatgaag aaggcggttg cggcgaacgc gaagatatcg aaggaggcga aggagacggt 180
gcaggagtgc gtgtcggagt tcatcagctt cataacagga gaggcttcg ataagtgcc 240
gaaggagaag aggaagacga tcaacggcga cgatcttctc tgggccatga ctaccctggg 300
cttcgaggac tacgtggatc ctctcaagat ttacctgcac aagtataggg agatggaggg 360
ggagaaaacc gctatgatgg gaaggccaca tgagagggat gagggttatg gccatggcca 420
tggtcatgca actcctatga tgacgatgat gatggggcat cagccccagc accagcacca 480
gcaccagcac caggacacg tgtatggatc tggatcagca tcttctgcaa gaactagata 540
gcatgtgtca tct 553

<210> 404
<211> 177
<212> PRT
<213> Glycine max

<220>
<223> G3474 polypeptide Orthologous to G481 and G482

<400> 404

Met Ala Glu Ser Asp Asn Glu Ser Gly Gly His Thr Gly Asn Ala Ser
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1           5           10           15
Gly Ser Asn Glu Leu Ser Gly Cys Arg Glu Gln Asp Arg Phe Leu Pro
      20           25           30
Ile Ala Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala
      35           40           45
Lys Ile Ser Lys Glu Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu
      50           55           60
Phe Ile Ser Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Lys Glu
      65           70           75           80
Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr
      85           90           95
Leu Gly Phe Glu Asp Tyr Val Asp Pro Leu Lys Ile Tyr Leu His Lys
      100          105          110
Tyr Arg Glu Met Glu Gly Glu Lys Thr Ala Met Met Gly Arg Pro His
      115          120          125
Glu Arg Asp Glu Gly Tyr Gly His Gly His Gly His Ala Thr Pro Met
      130          135          140
Met Thr Met Met Met Gly His Gln Pro Gln His Gln His Gln His Gln
      145          150          155          160
His Gln Gly His Val Tyr Gly Ser Gly Ser Ala Ser Ser Ala Arg Thr
      165          170          175

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Arg

<210> 405

<211> 600

<212> DNA

<213> Glycine max

<220>

<223> G3475 Predicted polypeptide sequence is orthologous to G481 and G482

<400> 405

tcgattatcc gtttgtcgat ggcggactcg gacaacgact ccggcggcgc gcacaacgcc 60

gggaagggga gcgagatgtc gccgcgggag caggaccggt tcctgccgat cgcgaacgtg 120

agccgcatca tgaagaaggc gctgccggcg aacgcgaaga tctcgaagga cgcgaaggag 180

acgggtgcagg agtgcggtgc ggagttcatc agcttcatca ccggcgaggc ctccgacaag 240

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tgccagcggg agaagcgcaa gacgatcaac ggcgacgacc tgctctgggc gatgaccact	300
ctcgggttcg aggactacgt cgagcctctc aagggctacc tccagcgctt ccgagaaatg	360
gaaggagaga agacagtggc ggcgcgtgac aaggacgcgc ctctctctac caatgctacc	420
aacagtgcct acgagagtcc tagttatgct gctgctcctg gtggaatcat gatgcatcag	480
ggacacgtgt acggttctgc cggcttccat caagtggctg gtggtgctat aaagggtggg	540
cctgtttatc ccgggcctgg atccaatgcc ggtaggccca ggtagatggg cctatgttat	600

<210> 406
 <211> 188
 <212> PRT
 <213> Glycine max

<220>
 <223> G3475 polypeptide Orthologous to G481 and G482

<400> 406

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1				5					10					15	

Gly	Ser	Glu	Met	Ser	Pro	Arg	Glu	Gln	Asp	Arg	Phe	Leu	Pro	Ile	Ala
			20					25					30		

Asn	Val	Ser	Arg	Ile	Met	Lys	Lys	Ala	Leu	Pro	Ala	Asn	Ala	Lys	Ile
		35					40					45			

Ser	Lys	Asp	Ala	Lys	Glu	Thr	Val	Gln	Glu	Cys	Val	Ser	Glu	Phe	Ile
	50					55					60				

Ser	Phe	Ile	Thr	Gly	Glu	Ala	Ser	Asp	Lys	Cys	Gln	Arg	Glu	Lys	Arg
65					70					75				80	

Lys	Thr	Ile	Asn	Gly	Asp	Asp	Leu	Leu	Trp	Ala	Met	Thr	Thr	Leu	Gly
				85					90					95	

Phe	Glu	Asp	Tyr	Val	Glu	Pro	Leu	Lys	Gly	Tyr	Leu	Gln	Arg	Phe	Arg
			100					105					110		

Glu	Met	Glu	Gly	Glu	Lys	Thr	Val	Ala	Ala	Arg	Asp	Lys	Asp	Ala	Pro
		115					120					125			

Pro	Pro	Thr	Asn	Ala	Thr	Asn	Ser	Ala	Tyr	Glu	Ser	Pro	Ser	Tyr	Ala
	130					135					140				

Ala	Ala	Pro	Gly	Gly	Ile	Met	Met	His	Gln	Gly	His	Val	Tyr	Gly	Ser
145					150					155					160

Ala Gly Phe His Gln Val Ala Gly Gly Ala Ile Lys Gly Gly Pro Val

165

170

175

Tyr Pro Gly Pro Gly Ser Asn Ala Gly Arg Pro Arg
180 185

<210> 407

<211> 528

<212> DNA

<213> Glycine max

<220>

<223> G3476 Predicted polypeptide sequence is orthologous to G481 and G482

<400> 407

ggattgattg tgaagatggc tgagtcggac aacgactcgg gaggggcgca gaacgcggga 60
aacagtggaa acttgagcga gttgtcgctt cgggaacagg accggtttct ccccatagcg 120
aacgtgagca ggatcatgaa gaaggccttg ccggcgaacg cgaagatctc gaaggacgcg 180
aaggagacgg tgcaggaatg cgtgtcggag ttcacagct tcataacggg tgaggcgctg 240
gacaagtgcc agagggagaa gcgcaagacc atcaacggcg acgatcttct ctgggccatg 300
acaaccctgg gattcgaaga gtacgtggag cctctgaaga ttacctcca gcgcttccgc 360
gagatggagg gagagaagac cgtggccgcc cgcgactctt ctaaggactc ggccctccgcc 420
tctctctatc atcagggaca cgtgtacggc tccctgcct accatcatca agtgccctggg 480
cccacttata ctgcccctgg tagaccaga tgacgtgctc ctctattc 528

<210> 408

<211> 165

<212> PRT

<213> Glycine max

<220>

<223> G3476 polypeptide Orthologous to G481 and G482

<400> 408

Met Ala Glu Ser Asp Asn Asp Ser Gly Gly Ala Gln Asn Ala Gly Asn
1 5 10 15

Ser Gly Asn Leu Ser Glu Leu Ser Pro Arg Glu Gln Asp Arg Phe Leu
20 25 30

Pro Ile Ala Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn
35 40 45

Ala Lys Ile Ser Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser
50 55 60

Glu Phe Ile Ser Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg
65 70 75 80

Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr
85 90 95

Thr Leu Gly Phe Glu Glu Tyr Val Glu Pro Leu Lys Ile Tyr Leu Gln
100 105 110

Arg Phe Arg Glu Met Glu Gly Glu Lys Thr Val Ala Ala Arg Asp Ser
115 120 125

Ser Lys Asp Ser Ala Ser Ala Ser Ser Tyr His Gln Gly His Val Tyr
130 135 140

Gly Ser Pro Ala Tyr His His Gln Val Pro Gly Pro Thr Tyr Pro Ala
145 150 155 160

Pro Gly Arg Pro Arg
165

<210> 409
<211> 568
<212> DNA
<213> Glycine max

<220>
<223> G3477 Predicted polypeptide sequence is orthologous to G481 and G482

<400> 409
tcgacttgta gggtttgtga gatgtcggat gcaccggcga gtccgagtca cgagagtggg 60
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cccattgcca acatcagccg catcatgaag aaggctctgc ctcccaatgg caagattgag 180
aaggatgcaa aagacacaat gcaagaatgc gtttctgaat tcatcagctt cattaccagc 240
gaggcgagtg agaaatgcca gaaggagaag agaaagacaa tcaatggaga cgatttacta 300
tgggccatgg caactttagg gtttgaagac tacattgagc cgcttaaggt gtacctggct 360
aggtacagag aggcggaggg tgacactaaa ggatctgcta gaagtgggtga tggatctgct 420
agaccagatc aagttggcct tgcaggtcaa aatgctcagc ttgttcatca gggttcgctg 480
aactatattg gtttgcaggt gcaaccacaa catctgggta tgccttcaat gcaaggccat 540
gaatagttta gatgcttcta cgcacgcg 568

<210> 410
<211> 174
<212> PRT
<213> Glycine max

<220>
<223> G3477 polypeptide Orthologous to G481 and G482

<400> 410

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Met Ser Asp Ala Pro Ala Ser Pro Ser His Glu Ser Gly Gly Glu Gln
1 5 10 15

Ser Pro Arg Gly Ser Leu Ser Gly Ala Ala Arg Glu Gln Asp Arg Tyr
20 25 30

Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala Leu Pro Pro
35 40 45

Asn Gly Lys Ile Ala Lys Asp Ala Lys Asp Thr Met Gln Glu Cys Val
50 55 60

Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Glu Lys Cys Gln
65 70 75 80

Lys Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met
85 90 95

Ala Thr Leu Gly Phe Glu Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu
100 105 110

Ala Arg Tyr Arg Glu Ala Glu Gly Asp Thr Lys Gly Ser Ala Arg Ser
115 120 125

Gly Asp Gly Ser Ala Arg Pro Asp Gln Val Gly Leu Ala Gly Gln Asn
130 135 140

Ala Gln Leu Val His Gln Gly Ser Leu Asn Tyr Ile Gly Leu Gln Val
145 150 155 160

Gln Pro Gln His Leu Val Met Pro Ser Met Gln Gly His Glu
165 170

<210> 411

<211> 602

<212> DNA

<213> Glycine max

<220>

<223> G3478 Predicted polypeptide sequence is orthologous to G481 and G482

<400> 411

ttccgtagt cgatggcgga ctccgacaac gactccggcg gcgcgcacaa cggcggaag 60

gggagcgaga tgtcgccg cgagcaggac cggtttctcc cgatcgcgaa cgtgagccgc 120

atcatgaaga aggcgctgcc ggcgaacgcg aagatctcga aggacgcgaa ggagacggtg 180

caggagtgcg tgtcagagtt catcagcttc atcaccggcg aggcctccga caagtgccag 240

cgcgagaagc gcaagacgat caacggcgac gacctgctct gggcgatgac cactctgggc 300

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ttcgaggact acgtggagcc tctcaaaggc tacctccagc gcttccgaga aatggaagga 360
gagaagaccg tggcggcgcg tgacaaggac gcgcctcctc ttacgaatgc taccaacagt 420
gcctacgaga gtgctaatta tgctgctgct gctgctgttc ctggtggaat catgatgcat 480
cagggacacg tgtacggttc tgccggcttc catcaagtgg ctggcggggc tataaagggt 540
gggcctgctt atcctggggc tggatccaat gccggtaggc ccagataaag agcctattat 600
ta 602

<210> 412
<211> 191
<212> PRT
<213> Glycine max

<220>
<223> G3478 polypeptide Orthologous to G481 and G482

<400> 412

Met Ala Asp Ser Asp Asn Asp Ser Gly Gly Ala His Asn Gly Gly Lys
1 5 10 15

Gly Ser Glu Met Ser Pro Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala
20 25 30

Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile
35 40 45

Ser Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile
50 55 60

Ser Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg
65 70 75 80

Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly
85 90 95

Phe Glu Asp Tyr Val Glu Pro Leu Lys Gly Tyr Leu Gln Arg Phe Arg
100 105 110

Glu Met Glu Gly Glu Lys Thr Val Ala Ala Arg Asp Lys Asp Ala Pro
115 120 125

Pro Leu Thr Asn Ala Thr Asn Ser Ala Tyr Glu Ser Ala Asn Tyr Ala
130 135 140

Ala Ala Ala Ala Val Pro Gly Gly Ile Met Met His Gln Gly His Val
145 150 155 160

Tyr Gly Ser Ala Gly Phe His Gln Val Ala Gly Gly Ala Ile Lys Gly

165

170

175

Gly Pro Ala Tyr Pro Gly Pro Gly Ser Asn Ala Gly Arg Pro Arg
180 185 190

<210> 413
<211> 803
<212> DNA
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3556 Predicted polypeptide sequence is orthologous to G1073

<400> 413
tcgacgggat ggggagcatc gacggccact cgctgcagca gcatcagggg tactcccacg 60
gcggcgggcgc gggagggagc aacgaggagg aggaggcgtc gccgccgccc ggcggtggct 120
cggctacggg gtcggcgggc cgccggccga gggggaggcc gccgggctcc aagaacaagc 180
cgaagccgcc cgctcgtggtg acgcgggaga gcccacacgc gatgcgttcc cacgtgctgg 240
agatcgccag cggcgccgac atcgtcgagg ccacgcggg cttctcccgc cgcaggcagc 300
gcggcggtctc cgtgctcagc gggagcgggc ccgtcaccaa cgtcacgctc cggcagcccg 360
cggggactgg ggccgccgcc gtcgcgctgc gggggagggt cgagatattg tccatgtctg 420
gcgccttctt cccggcgccc gcgcccagc gggccacggg gctcgccgtg tacctcgccg 480
gcggggcaggg gcaggtggtg ggtgggagcg tcatggggga gctgatcgcg tcgggccccg 540
tcatggtgat cgcgccacg ttcggcaacg ccacgtacga gaggctgccg ctggaccagg 600
aaggcgagga gggcgccgtg ctgtccgggt cggagggcgc cgccgcgcag atggagcagc 660
agagcagcgg aggcgccgctc gtgccccgc cgatgtacgc cgccgtccag cagacgccgc 720
cgcacgacat gttcgggcag tgggggcatg cagcgggtggc tcggccgccg ccgacatcgt 780
tctagcactg gcaccggtta att 803

<210> 414
<211> 258
<212> PRT
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3556 polypeptide Orthologous to G1073

<400> 414

Met Gly Ser Ile Asp Gly His Ser Leu Gln Gln His Gln Gly Tyr Ser
1 5 10 15

His Gly Gly Gly Ala Gly Gly Ser Asn Glu Glu Glu Glu Ala Ser Pro
20 25 30

Pro Pro Gly Gly Gly Ser Ala Thr Gly Ser Ala Gly Arg Arg Pro Arg

35

40

45

Gly Arg Pro Pro Gly Ser Lys Asn Lys Pro Lys Pro Pro Val Val Val
50 55 60

Thr Arg Glu Ser Pro Asn Ala Met Arg Ser His Val Leu Glu Ile Ala
65 70 75 80

Ser Gly Ala Asp Ile Val Glu Ala Ile Ala Gly Phe Ser Arg Arg Arg
85 90 95

Gln Arg Gly Val Ser Val Leu Ser Gly Ser Gly Ala Val Thr Asn Val
100 105 110

Thr Leu Arg Gln Pro Ala Gly Thr Gly Ala Ala Ala Val Ala Leu Arg
115 120 125

Gly Arg Phe Glu Ile Leu Ser Met Ser Gly Ala Phe Leu Pro Ala Pro
130 135 140

Ala Pro Pro Gly Ala Thr Gly Leu Ala Val Tyr Leu Ala Gly Gly Gln
145 150 155 160

Gly Gln Val Val Gly Gly Ser Val Met Gly Glu Leu Ile Ala Ser Gly
165 170 175

Pro Val Met Val Ile Ala Ala Thr Phe Gly Asn Ala Thr Tyr Glu Arg
180 185 190

Leu Pro Leu Asp Gln Glu Gly Glu Glu Gly Ala Val Leu Ser Gly Ser
195 200 205

Glu Gly Ala Ala Ala Gln Met Glu Gln Gln Ser Ser Gly Gly Ala Val
210 215 220

Val Pro Pro Pro Met Tyr Ala Ala Val Gln Gln Thr Pro Pro His Asp
225 230 235 240

Met Phe Gly Gln Trp Gly His Ala Ala Val Ala Arg Pro Pro Pro Thr
245 250 255

Ser Phe

<210> 415

<211> 435

<212> DNA

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3835 Predicted polypeptide sequence is orthologous to G481 and G482

<400> 415

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acggagtcca tcagcttcgt caccggcgag gcgtcggagc ggtgccggcg ggagcggcgg      180
aagacggtga acggcgacga cgtctgccac gccatgagga gcctcggcct cgaccactac      240
gccgacgcca tgcacaggta cctgcagagg taccgcgagg gcgaggagct cgccgcgtcg      300
ctcaacagca gcagcagcgc cgccgccgcc gccgccgccg ccggcagcag gggcggtggc      360
gccatacaga tcgacgtgag agctgagctc tccatcttca gatcaggcaa caaccaaggt      420
cgtccaaaca attaa                                         435
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<210> 416

<211> 144

<212> PRT

<213> Oryza sativa (japonica cultivar-group)

<220>

<223> G3835 polypeptide Orthologous to G481 and G482

<400> 416

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Met Thr Asn Gly Gln Asp Asn Leu Leu Pro Ile Ala Asn Val Gly Arg
1           5           10           15
```

```
Ile Met Lys Asp Gly Leu Pro Pro Gln Ala Lys Ile Ser Lys Arg Ala
20           25           30
```

```
Lys Glu Thr Ile Gln Glu Cys Ala Thr Glu Phe Ile Ser Phe Val Thr
35           40           45
```

```
Gly Glu Ala Ser Glu Arg Cys Arg Arg Glu Arg Arg Lys Thr Val Asn
50           55           60
```

```
Gly Asp Asp Val Cys His Ala Met Arg Ser Leu Gly Leu Asp His Tyr
65           70           75           80
```

```
Ala Asp Ala Met His Arg Tyr Leu Gln Arg Tyr Arg Glu Gly Glu Glu
85           90           95
```

```
Leu Ala Ala Ser Leu Asn Ser Ser Ser Ser Ala Ala Ala Ala Ala Ala
100          105          110
```

```
Ala Ala Gly Ser Arg Gly Gly Gly Ala Ile Gln Ile Asp Val Arg Ala
115          120          125
```

```
Glu Leu Ser Ile Phe Arg Ser Gly Asn Asn Gln Gly Arg Pro Asn Asn
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130

135

140

<210> 417
<211> 534
<212> DNA
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3836 Predicted polypeptide sequence is orthologous to G481 and G482

<400> 417
atggccgacc accatggcgg ccaccacgcc gacgggcacg gccggcagca gcagctgcag 60
ggggaggcgg cggatcaggc ggcgggcggag atcatcaagg agcaggacag gttgctgcca 120
atcggaacg tggggcgaat catgaagcag atcctcccc ccaacgcca gatctccaag 180
gaggccaagg agacgatgca ggagtgcgtc tcggagttca tcagcttcgt caccggcgag 240
gcctccgaca agtgccacaa ggagaagcgc aagacggtca acggcgacga cgtctgctgg 300
gccttcggcg ccctcggctt cgacgactac gtcgacccca tgcgcaggta cctcaacaag 360
taccgcgagc tcgagggcga ccgcgccgcc gccgcgccca cctcccgtc cggcgccggc 420
gccgcgcggg gccccgacca cccttcctcc tcctcctccg ccgccgccgc caccgccggt 480
catttcatgt tcaacgccat ggacaggtcg acggatagct ccaggcagtt ctag 534

<210> 418
<211> 177
<212> PRT
<213> Oryza sativa (japonica cultivar-group)

<220>
<223> G3836 polypeptide Orthologous to G481 and G482

<400> 418
Met Ala Asp His His Gly Gly His His Ala Asp Gly His Arg Arg Gln
1 5 10 15
Gln Gln Leu Gln Gly Glu Ala Ala Asp Gln Ala Ala Ala Glu Ile Ile
20 25 30
Lys Glu Gln Asp Arg Leu Leu Pro Ile Ala Asn Val Gly Arg Ile Met
35 40 45
Lys Gln Ile Leu Pro Pro Asn Ala Lys Ile Ser Lys Glu Ala Lys Glu
50 55 60
Thr Met Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr Gly Glu
65 70 75 80
Ala Ser Asp Lys Cys His Lys Glu Lys Arg Lys Thr Val Asn Gly Asp
85 90 95

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Asp Val Cys Trp Ala Phe Gly Ala Leu Gly Phe Asp Asp Tyr Val Asp
100 105 110

Pro Met Arg Arg Tyr Leu Asn Lys Tyr Arg Glu Leu Glu Gly Asp Arg
115 120 125

Ala Ala Ala Ala Ala Thr Ser Arg Ser Gly Ala Gly Ala Ala Ala Gly
130 135 140

Pro Asp His Pro Ser Ser Ser Ser Ser Ala Ala Ala Ala Thr Ala Gly
145 150 155 160

His Phe Met Phe Asn Ala Met Asp Arg Ser Thr Asp Ser Ser Arg Gln
165 170 175

Phe

<210> 419
<211> 795
<212> DNA
<213> Glycine max

<220>
<223> G3837 Predicted polypeptide sequence is orthologous to G481 and G482

<400> 419
ctgtgtttga gaggactaaa gtaaacagat gggtgacaac aacataggca aagtcttaga 60
gagagaaggc tttaagtaca acttcacggc agctgcaagt gacacctctg cacaagatga 120
ggtgattaaa gagcaagatc ggttgcttcc aatagcaaat gtggggcgca tcatgaagca 180
aatccttcct cctaacgcca agatctcaaa ggaagctaaa gaaaccatgc aagaatgtgt 240
gtccgagttc attagctttg tcactgggga agcttctgac aagtgtcaca aggagaagcg 300
caagaccgtg aatggcgacg atatttgctg ggcccttgct accctagggt ttgatgacta 360
ctctgagcca cttaaaagggt acttgcataa gtataggagg ttcgaagggg agagagcaaa 420
tcaaaataag ggtaacaaca acacttatga aaacaacatt gcaaacatat aaattaatta 480
tgtggaagggt gaactctttc tccaattccc atgatcaatg tgattgatag ttgttaatct 540
gatcttctag ttttctcctg aatttgagat actcaagggg cttgtatcct tatgtgatat 600
atatatgacg tgagtcatgt atgcaaactc acgtgtttta gacctgatat tttcatcaag 660
ggttgaaatt accctagatg aacacatggg agcttgagaa tcatgtgagt tacaactaat 720
ctttgtattt gtctatccaa taataagctt ggatcctttc cagaaaaaaaa aaaaaaaaaa 780
aaaaaaaaaa aaaaaa 795

<210> 420

<211> 147
<212> PRT
<213> Glycine max

<220>
<223> G3837 polypeptide Orthologous to G481 and G482

<400> 420

Met Gly Asp Asn Asn Ile Gly Lys Val Leu Glu Arg Glu Gly Phe Lys
1 5 10 15

Tyr Asn Phe Thr Ala Ala Ala Ser Asp Thr Ser Ala Gln Asp Glu Val
20 25 30

Ile Lys Glu Gln Asp Arg Leu Leu Pro Ile Ala Asn Val Gly Arg Ile
35 40 45

Met Lys Gln Ile Leu Pro Pro Asn Ala Lys Ile Ser Lys Glu Ala Lys
50 55 60

Glu Thr Met Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr Gly
65 70 75 80

Glu Ala Ser Asp Lys Cys His Lys Glu Lys Arg Lys Thr Val Asn Gly
85 90 95

Asp Asp Ile Cys Trp Ala Leu Ala Thr Leu Gly Phe Asp Asp Tyr Ser
100 105 110

Glu Pro Leu Lys Arg Tyr Leu His Lys Tyr Arg Glu Phe Glu Gly Glu
115 120 125

Arg Ala Asn Gln Asn Lys Gly Asn Asn Asn Thr Tyr Glu Asn Asn Ile
130 135 140

Ala Asn Ile
145

<210> 421
<211> 929
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> CBF1

<400> 421
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agacagatat actatctttt attaatccaa aaagactgag aactctagta actacgtact 120
acttaaacct tatccagttt cttgaaacag agtactctga tcaatgaact cattttcagc 180

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tttttctgaa atgtttggct ccgattacga gcctcaaggc ggagattatt gtccgacgtt      240
ggccaacgagt tgtccgaaga aaccggcggg ccgtaagaag ttctgtgaga ctctgcaccc      300
aatttacaga ggagttcgtc aaagaaactc cggtaagtgg gtttctgaag tgagagagcc      360
aaacaagaaa accaggattt ggctcgggac tttccaaacc gctgagatgg cagctcgtgc      420
tcacgacgtc gctgcattag ccctccgtgg ccgatcagca tgtctcaact tcgctgactc      480
ggcttggcgg ctacgaatcc cggagtcaac atgcgccaaag gatatccaaa aagcggctgc      540
tgaagcggcg ttggcttttc aagatgagac gtgtgatacg acgaccacga atcatggcct      600
ggacatggag gagacgatgg tggaagctat ttatacaccg gaacagagcg aaggtgcgtt      660
ttatatggat gaggagacaa tgtttgggat gccgactttg ttggataata tggctgaagg      720
catgctttta ccgccgccgt ctgttcaatg gaatcataat tatgacggcg aaggagatgg      780
tgacgtgtcg ctttggagtt actaatattc gatagtcgtt tccatttttg tactatagtt      840
tgaaaatatt ctagttcctt tttttagaat ggttccttca ttttatttta ttttattggt      900
gtagaaacga gtggaaaata attcaatac      929

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<210> 422
 <211> 213
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <223> CBF1 polypeptide

<400> 422

Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu
 1 5 10 15

Pro Gln Gly Gly Asp Tyr Cys Pro Thr Leu Ala Thr Ser Cys Pro Lys
 20 25 30

Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His Pro Ile Tyr
 35 40 45

Arg Gly Val Arg Gln Arg Asn Ser Gly Lys Trp Val Ser Glu Val Arg
 50 55 60

Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe Gln Thr Ala
 65 70 75 80

Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala Leu Arg Gly
 85 90 95

Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile
 100 105 110

MBI0058CIP.ST25.txt

Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala Ala Glu Ala
115 120 125

Ala Leu Ala Phe Gln Asp Glu Thr Cys Asp Thr Thr Thr Thr Asn His
130 135 140

Gly Leu Asp Met Glu Glu Thr Met Val Glu Ala Ile Tyr Thr Pro Glu
145 150 155 160

Gln Ser Glu Gly Ala Phe Tyr Met Asp Glu Glu Thr Met Phe Gly Met
165 170 175

Pro Thr Leu Leu Asp Asn Met Ala Glu Gly Met Leu Leu Pro Pro Pro
180 185 190

Ser Val Gln Trp Asn His Asn Tyr Asp Gly Glu Gly Asp Gly Asp Val
195 200 205

Ser Leu Trp Ser Tyr
210

<210> 423
<211> 803
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> CBF2

<400> 423
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gggaaggaag aagtttcgtg agactcgtca cccaatttac agaggagttc gtcaaagaaa 180
ctccggtaag tgggtgtgtg agttgagaga gccaaacaag aaaacgagga tttggctcgg 240
gactttccaa accgctgaga tggcagctcg tgctcacgac gtcgccgcca tagctctccg 300
tggcagatct gcctgtctca atttcgctga ctcggttggt cggtacgaa tcccggaatc 360
aacctgtgcc aaggaaatcc aaaaggcggc ggctgaagcc gcgttgaatt ttcaagatga 420
gatgtgtcat atgacgacgg atgctcatgg tcttgacatg gaggagacct tgggtggaggc 480
tatttatacg ccggaacaga gccaagatgc gttttatatg gatgaagagg cgatgttggg 540
gatgtctagt ttgttgata acatggccga agggatgctt ttaccgtcgc cgtcggttca 600
atggaactat aattttgatg tcgagggaga tgatgacgtg tccttatgga gctattaaaa 660
ttcgattttt atttccattt ttggtattat agctttttat acatttgatc cttttttaga 720
atggatcttc ttcttttttt gggtgtgaga aacgaatgta aatggtaaaa gttgttgtca 780

aatgcaaag tttttgagtg cag

<210> 424

<211> 207

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> CBF2 polypeptide

<400> 424

Met Phe Gly Ser Asp Tyr Glu Ser Pro Val Ser Ser Gly Gly Asp Tyr
 1 5 10 15

Ser Pro Lys Leu Ala Thr Ser Cys Pro Lys Lys Pro Ala Gly Arg Lys
 20 25 30

Lys Phe Arg Glu Thr Arg His Pro Ile Tyr Arg Gly Val Arg Gln Arg
 35 40 45

Asn Ser Gly Lys Trp Val Cys Glu Leu Arg Glu Pro Asn Lys Lys Thr
 50 55 60

Arg Ile Trp Leu Gly Thr Phe Gln Thr Ala Glu Met Ala Ala Arg Ala
 65 70 75 80

His Asp Val Ala Ala Ile Ala Leu Arg Gly Arg Ser Ala Cys Leu Asn
 85 90 95

Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile Pro Glu Ser Thr Cys Ala
 100 105 110

Lys Glu Ile Gln Lys Ala Ala Ala Glu Ala Ala Leu Asn Phe Gln Asp
 115 120 125

Glu Met Cys His Met Thr Thr Asp Ala His Gly Leu Asp Met Glu Glu
 130 135 140

Thr Leu Val Glu Ala Ile Tyr Thr Pro Glu Gln Ser Gln Asp Ala Phe
 145 150 155 160

Tyr Met Asp Glu Glu Ala Met Leu Gly Met Ser Ser Leu Leu Asp Asn
 165 170 175

Met Ala Glu Gly Met Leu Leu Pro Ser Pro Ser Val Gln Trp Asn Tyr
 180 185 190

Asn Phe Asp Val Glu Gly Asp Asp Asp Val Ser Leu Trp Ser Tyr
 195 200 205

<210> 425
 <211> 908
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> misc_feature
 <222> (851)..(851)
 <223> n is a, c, g, or t

<220>
 <223> CBF3

<400> 425
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 gaactcattt tctgcttttt ctgaaatggt tggctccgat tacgagtctt cggtttcctc 180
 aggcggtgat tatattccga cgcttgcgag cagctgcccc aagaaaccgg cgggtcgtaa 240
 gaagtttcgt gagactcgtc acccaatata cagaggaggt cgtcggagaa actccggtaa 300
 gtgggtttgt gaggttagag aaccaaacia gaaaacaagg atttggtctg gaacatttca 360
 aaccgctgag atggcagctc gagctcacga cgttgccgct ttagcccttc gtggccgatc 420
 agcctgtctc aatttcgctg actcggcttg gagactccga atcccggaat caacttgctc 480
 taaggacatc caaaaggcgg cggctgaagc tgcgttggcg tttcaggatg agatgtgtga 540
 tgcgacgacg gatcatggct tcgacatgga ggagacgttg gtggaggcta ttacacggc 600
 ggaacagagc gaaaatgcgt tttatatgca cgatgaggcg atgtttgaga tgccgagttt 660
 gttggctaata atggcagaag ggatgctttt gccgcttccg tccgtacagt ggaatcataa 720
 tcatgaagtc gacggcgatg atgacgacgt atcgttatgg agttattaaa actcagatta 780
 ttatttccat ttttagtacg atacttttta ttttattatt atttttagat ctttttttag 840
 aatggaatct ncattatggt tgtaaaactg agaaacgagt gtaaattaaa ttgattcagt 900
 ttcagtat 908

<210> 426
 <211> 216
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Ser Ser Val Ser Ser Gly Gly Asp Tyr Ile Pro Thr Leu Ala Ser Ser
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20

25

30

Cys Pro Lys Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His
35 40 45

Pro Ile Tyr Arg Gly Val Arg Arg Arg Asn Ser Gly Lys Trp Val Cys
50 55 60

Glu Val Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe
65 70 75 80

Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala
85 90 95

Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg
100 105 110

Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala
115 120 125

Ala Glu Ala Ala Leu Ala Phe Gln Asp Glu Met Cys Asp Ala Thr Thr
130 135 140

Asp His Gly Phe Asp Met Glu Glu Thr Leu Val Glu Ala Ile Tyr Thr
145 150 155 160

Ala Glu Gln Ser Glu Asn Ala Phe Tyr Met His Asp Glu Ala Met Phe
165 170 175

Glu Met Pro Ser Leu Leu Ala Asn Met Ala Glu Gly Met Leu Leu Pro
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Leu Pro Ser Val Gln Trp Asn His Asn His Glu Val Asp Gly Asp Asp
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Asp Asp Val Ser Leu Trp Ser Tyr
210 215

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Cys Glu Val Arg Glu Pro Asn Lys Lys Ser Arg Ile Trp Leu Gly Thr
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Phe Lys Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu
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Ala Leu Arg Gly Arg Gly Ala Cys Leu Asn Tyr Ala Asp Ser Ala Trp
50          55          60

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Arg Leu Arg Ile Pro Glu Thr Thr Cys His Lys Asp Ile Gln Lys Ala
65          70          75          80

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Ala Ala Glu Ala Ala Leu Ala Phe Glu Ala Glu Lys Ser Asp Val Thr
85          90          95

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Met Gln Asn Gly Gln Asn Met Glu Glu Thr Thr Ala Val Ala Ser Gln
100         105         110

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Ala Glu Val Asn Asp Thr Thr Thr Glu His Gly Met Asn Met Glu Glu
115         120         125

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Ala Thr Ala Val Ala Ser Gln Ala Glu Val Asn Asp Thr Thr Thr Asp
130         135         140

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His Gly Val Asp Met Glu Glu Thr Met Val Glu Ala Val Phe Thr Gly
145 150 155 160

Glu Gln Ser Glu Gly Phe Asn Met Ala Lys Glu Ser Thr Val Glu Ala
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Ala Val Val Thr Glu Glu Pro Ser Lys Gly Ser Tyr Met Asp Glu Glu
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Trp Met Leu Glu Met Pro Thr Leu Leu Ala Asp Met Ala Glu Gly Met
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